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SEQUENCE LISTING

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<120> MUTATIONS IN THE DIABETES SUSCEPTIBILITY GENES  
HEPATOCTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNG-1BETA AND  
HNF-4ALPHA

<130> ARCD:272USC1

<140> 09/754,106  
<141> 2001-03-01

<150> 08/927,219  
<151> 1997-09-09

<150> 60/029,679  
<151> 1996-10-30

<150> 60/028,056  
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<170> PatentIn Ver. 2.1

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Primer

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Thr Glu Leu Leu Ala Ala Leu Leu Glu Ser Gly Leu Ser Lys Glu Ala  
10 15 20 25

CTG ATC CAG GCA CTG GGT GAG CCG GGG CCC TAC CTC CTG GCT GGA GAA 146  
Leu Ile Gln Ala Leu Gly Glu Pro Gly Pro Tyr Leu Leu Ala Gly Glu  
30 35 40

GGC CCC CTG GAC AAG GGG GAG TCC TGC GGC GGC GGT CGA GGG GAG CTG 194  
Gly Pro Leu Asp Lys Gly Glu Ser Cys Gly Gly Gly Arg Gly Glu Leu  
45 50 55

GCT GAG CTG CCC AAT GGG CTG GGG GAG ACT CGG GGC TCC GAG GAC GAG 242  
Ala Glu Leu Pro Asn Gly Leu Gly Glu Thr Arg Gly Ser Glu Asp Glu  
60 65 70

ACG GAC GAC GAT GGG GAA GAC TTC ACG CCA CCC ATC CTC AAA GAG CTG 290  
Thr Asp Asp Asp Gly Glu Asp Phe Thr Pro Pro Ile Leu Lys Glu Leu  
75 80 85

GAG AAC CTC AGC CCT GAG GAG GCG GCC CAC CAG AAA GCC GTG GTG GAG 338  
Glu Asn Leu Ser Pro Glu Glu Ala Ala His Gln Lys Ala Val Val Glu  
90 95 100 105

ACC CTT CTG CAG GAG GAC CCG TGG CGT GTG GCG AAG ATG GTC AAG TCC 386  
Thr Leu Leu Gln Glu Asp Pro Trp Arg Val Ala Lys Met Val Lys Ser  
110 115 120

TAC CTG CAG CAG CAC AAC ATC CCA CAG CGG GAG GTG GTC GAT ACC ACT 434  
Tyr Leu Gln Gln His Asn Ile Pro Gln Arg Glu Val Val Asp Thr Thr  
125 130 135

GGC CTC AAC CAG TCC CAC CTG TCC CAA CAC CTC AAC AAG GGC ACT CCC 482  
Gly Leu Asn Gln Ser His Leu Ser Gln His Leu Asn Lys Gly Thr Pro  
140 145 150

ATG AAG ACG CAG AAG CGG GCC GCC CTG TAC ACC TGG TAC GTC CGC AAG 530  
Met Lys Thr Gln Lys Arg Ala Ala Leu Tyr Thr Trp Tyr Val Arg Lys  
155 160 165

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Gln Arg Glu Val Ala Gln Gln Phe Thr His Ala Gly Gln Gly Gly Leu  
170 175 180 185

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Ile Glu Glu Pro Thr Gly Asp Glu Leu Pro Thr Lys Lys Gly Arg Arg  
190 195 200

AAC CGT TTC AAG TGG GGC CCA GCA TCC CAG CAG ATC CTG TTC CAG GCC 674  
Asn Arg Phe Lys Trp Gly Pro Ala Ser Gln Gln Ile Leu Phe Gln Ala  
205 210 215

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GAG GAG TGC AAT AGG GCG GAA TGC ATC CAG AGA GGG GTG TCC CCA TCA Glu Glu Cys Asn Arg Ala Glu Cys Ile Gln Arg Gly Val Ser Pro Ser 235 240 245	770
CAG GCA CAG GGG CTG GGC TCC AAC CTC GTC ACG GAG GTG CGT GTC TAC Gln Ala Gln Gly Leu Gly Ser Asn Leu Val Thr Glu Val Arg Val Tyr 250 255 260 265	818
AAC TGG TTT GCC AAC CGG CGC AAA GAA GAA GCC TTC CGG CAC AAG CTG Asn Trp Phe Ala Asn Arg Arg Lys Glu Glu Ala Phe Arg His Lys Leu 270 275 280	866
GCC ATG GAC ACG TAC AGC GGG CCC CCC CCA GGG CCA GGC CCG GGA CCT Ala Met Asp Thr Tyr Ser Gly Pro Pro Pro Gly Pro Gly Pro Gly Pro 285 290 295	914
GCG CTG CCC GCT CAC AGC TCC CCT GGC CTG CCT CCA CCT GCC CTC TCC Ala Leu Pro Ala His Ser Ser Pro Gly Leu Pro Pro Pro Ala Leu Ser 300 305 310	962
CCC AGT AAG GTC CAC GGT GTG CGC TNT GGA CAG CCT GCG ACC AGT GAG Pro Ser Lys Val His Gly Val Arg Gly Gln Pro Ala Thr Ser Glu 315 320 325	1010
ACT GCA GAA GTA CCC TCA AGC AGC GGC GGT CCC TTA GTG ACA GTG TCT Thr Ala Glu Val Pro Ser Ser Ser Gly Gly Pro Leu Val Thr Val Ser 330 335 340	1058
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CTG CTG AGT ACA GAA GCC AAG CTG GTC TCA GCA GCT GGG GGC CCC CTC Leu Leu Ser Thr Glu Ala Lys Leu Val Ser Ala Ala Gly Gly Pro Leu 365 370 375	1154
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CAG CCG CTC ATG CCA CCT GTG CAG AGC CAT GTG ACC CAG AGC CCC TTC Gln Pro Leu Met Pro Pro Val Gln Ser His Val Thr Gln Ser Pro Phe 475 480 485	1490
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CCCGTGGAGG CTGCTCGGGG TGCACAGGAG GGGGTCGTGG AGAGCTAGGA GCAAAGCCTG	2156
TTCATGGCAG ATGTAGGAGG GACTGTGCT GCTTCGTGGG ATACAGTCTT CTTACTTGGA	2216

ACTGAAGGGG GCGGCCTATG ACTTGGGCAC CCCAGCCTG GGCCTATGGA GAGCCCTGGG	2276
ACCGCTACAC CACTCTGGCA GCCACACTTC TCAGGACACA GGCCTGTGTA GCTGTGACCT	2336
GCTGAGCTCT GAGAGGCCCT GGATCAGCGT GGCCTTGTTT TGTCACCAAT GTACCCACCG	2396
GGCCACTCCT TCCTGCCCCA ACTCCTTCCA GCTAGTGACC CACATGCCAT TTGTACTGAC	2456
CCCATCACCT ACTCACACAG GCATTTCTTG GGTGGCTACT CTGTGCCAGA GCCTGGGGCT	2516
CTAACTGCCT GAGCCCAGGG AGGCCGAAGC TAACAGGGAA GGCAGGCAGG GCTCTCTTGG	2576
TCTTCCCATC CCCAGCGATT CCCTCTCCCA GGGCCCATGA CCTCCAGCTT TCCTGTATTT	2636
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ACTTCGGGGC TGGGAAGTCG TCCTTACTCC TGTGGGAGCC TCGCAACCCG TGCCAAGTCC	2756
AGGTCCTGGT GGGGCAGCTC CTCTGTCTCG AGCGCCCTGC AGACCCTGCC CTTGTTTGGG	2816
GCAGGAGTAG CTGAGCTCAC AAGGCAGCAA GGGCCGAGCA GCTGAGCAGG GCCGGGGAAC	2876
TGGCCAAGCT GAGGTGCCCA GGAGAAGAAA GAGGTGACCC CAGGGCACAG GAGCTACCTG	2936
TGTGGACAGG ACTAACACTC AGAAGCCTGG GTGCCTGGCT GGCTGAGGGC AGTTCGCAGC	2996
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GCGTCTACCC TGGGATTAG GAAAAGGCCT GGGGTGACCC GGCACCCCCT GCAGCTTGTA	3176
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			20					25					30		

Pro	Gly	Pro	Tyr	Leu	Leu	Ala	Gly	Glu	Gly	Pro	Leu	Asp	Lys	Gly	Glu
			35				40					45			

Ser Cys Gly Gly Gly Arg Gly Glu Leu Ala Glu Leu Pro Asn Gly Leu  
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 Gly Glu Thr Arg Gly Ser Glu Asp Glu Thr Asp Asp Asp Gly Glu Asp  
 65 70 75 80  
 Phe Thr Pro Pro Ile Leu Lys Glu Leu Glu Asn Leu Ser Pro Glu Glu  
 85 90 95  
 Ala Ala His Gln Lys Ala Val Val Glu Thr Leu Leu Gln Glu Asp Pro  
 100 105 110  
 Trp Arg Val Ala Lys Met Val Lys Ser Tyr Leu Gln Gln His Asn Ile  
 115 120 125  
 Pro Gln Arg Glu Val Val Asp Thr Thr Gly Leu Asn Gln Ser His Leu  
 130 135 140  
 Ser Gln His Leu Asn Lys Gly Thr Pro Met Lys Thr Gln Lys Arg Ala  
 145 150 155 160  
 Ala Leu Tyr Thr Trp Tyr Val Arg Lys Gln Arg Glu Val Ala Gln Gln  
 165 170 175  
 Phe Thr His Ala Gly Gln Gly Gly Leu Ile Glu Glu Pro Thr Gly Asp  
 180 185 190  
 Glu Leu Pro Thr Lys Lys Gly Arg Arg Asn Arg Phe Lys Trp Gly Pro  
 195 200 205  
 Ala Ser Gln Gln Ile Leu Phe Gln Ala Tyr Glu Arg Gln Lys Asn Pro  
 210 215 220  
 Ser Lys Glu Glu Arg Glu Thr Leu Val Glu Glu Cys Asn Arg Ala Glu  
 225 230 235 240  
 Cys Ile Gln Arg Gly Val Ser Pro Ser Gln Ala Gln Gly Leu Gly Ser  
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 Asn Leu Val Thr Glu Val Arg Val Tyr Asn Trp Phe Ala Asn Arg Arg  
 260 265 270  
 Lys Glu Glu Ala Phe Arg His Lys Leu Ala Met Asp Thr Tyr Ser Gly  
 275 280 285  
 Pro Pro Pro Gly Pro Gly Pro Gly Pro Ala Leu Pro Ala His Ser Ser  
 290 295 300  
 Pro Gly Leu Pro Pro Pro Ala Leu Ser Pro Ser Lys Val His Gly Val  
 305 310 315 320  
 Arg Gly Gln Pro Ala Thr Ser Glu Thr Ala Glu Val Pro Ser Ser Ser  
 325 330 335  
 Gly Gly Pro Leu Val Thr Val Ser Thr Pro Leu His Gln Val Ser Pro  
 340 345 350

Thr Gly Leu Glu Pro Ser His Ser Leu Leu Ser Thr Glu Ala Lys Leu  
 355 360 365  
 Val Ser Ala Ala Gly Gly Pro Leu Pro Pro Val Ser Thr Leu Thr Ala  
 370 375 380  
 Leu His Ser Leu Glu Gln Thr Ser Pro Gly Leu Asn Gln Gln Pro Gln  
 385 390 395 400  
 Asn Leu Ile Met Ala Ser Leu Pro Gly Val Met Thr Ile Gly Pro Gly  
 405 410 415  
 Glu Pro Ala Ser Leu Gly Pro Thr Phe Thr Asn Thr Gly Ala Ser Thr  
 420 425 430  
 Leu Val Ile Gly Leu Ala Ser Thr Gln Ala Gln Ser Val Pro Val Ile  
 435 440 445  
 Asn Ser Met Gly Ser Ser Leu Thr Thr Leu Gln Pro Val Gln Phe Ser  
 450 455 460  
 Gln Pro Leu His Pro Ser Tyr Gln Gln Pro Leu Met Pro Pro Val Gln  
 465 470 475 480  
 Ser His Val Thr Gln Ser Pro Phe Met Ala Thr Met Ala Gln Leu Gln  
 485 490 495  
 Ser Pro His Ala Leu Tyr Ser His Lys Pro Glu Val Ala Gln Tyr Thr  
 500 505 510  
 His Thr Gly Leu Leu Pro Gln Thr Met Leu Ile Thr Asp Thr Thr Asn  
 515 520 525  
 Leu Ser Ala Leu Ala Ser Leu Thr Pro Thr Lys Gln Val Phe Thr Ser  
 530 535 540  
 Asp Thr Glu Ala Ser Ser Glu Ser Gly Leu His Thr Pro Ala Ser Gln  
 545 550 555 560  
 Ala Thr Thr Leu His Val Pro Ser Gln Asp Pro Ala Gly Ile Gln His  
 565 570 575  
 Leu Gln Pro Ala His Arg Leu Ser Ala Ser Pro Thr Val Ser Ser Ser  
 580 585 590  
 Ser Leu Val Leu Tyr Gln Ser Ser Asp Ser Ser Asn Gly Gln Ser His  
 595 600 605  
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Met Val Ser Lys Leu Ser Gln Leu Gln  
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ACG GAG CTC CTG GCG GCC CTG CTC GAG TCA GGG CTG AGC AAA GAG GCA 98  
Thr Glu Leu Leu Ala Ala Leu Leu Glu Ser Gly Leu Ser Lys Glu Ala  
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CTG ATC CAG GCA CTG GGT GAG CCG GGG CCC TAC CTC CTG GCT GGA GAA 146  
Leu Ile Gln Ala Leu Gly Glu Pro Gly Pro Tyr Leu Leu Ala Gly Glu  
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GGC CCC CTG GAC AAG GGG GAG TCC TGC GGC GGC GGT CGA GGG GAG CTG 194  
Gly Pro Leu Asp Lys Gly Glu Ser Cys Gly Gly Gly Arg Gly Glu Leu  
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GCT GAG CTG CCC AAT GGG CTG GGG GAG ACT CGG GGC TCC GAG GAC GAG 242  
Ala Glu Leu Pro Asn Gly Leu Gly Glu Thr Arg Gly Ser Glu Asp Glu  
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ACG GAC GAC GAT GGG GAA GAC TTC ACG CCA CCC ATC CTC AAA GAG CTG 290  
Thr Asp Asp Asp Gly Glu Asp Phe Thr Pro Pro Ile Leu Lys Glu Leu  
75 80 85

GAG AAC CTC AGC CCT GAG GAG GCG GCC CAC CAG AAA GCC GTG GTG GAG 338  
Glu Asn Leu Ser Pro Glu Glu Ala Ala His Gln Lys Ala Val Val Glu  
90 95 100 105

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110 115 120

TAC CTG CAG CAG CAC AAC ATC CCA CAG CAG GAG GTG GTC GAT ACC ACT 434  
Tyr Leu Gln Gln His Asn Ile Pro Gln Gln Glu Val Val Asp Thr Thr  
125 130 135

GGC CTC AAC CAG TCC CAC CTG TCC CAA CAC CTC AAC AAG GGC ACT CCC 482



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Met	Lys	Thr	Gln	Lys	Arg	Ala	Ala	Leu	Tyr	Thr	Trp	Tyr	Val	Arg	Lys		
	155					160					165						
CAG	CGA	GAG	GTG	GCG	CAG	CAG	TTC	ACC	CAT	GCA	GGG	CAG	GGA	GGG	CTG	578	
Gln	Arg	Glu	Val	Ala	Gln	Gln	Phe	Thr	His	Ala	Gly	Gln	Gly	Gly	Leu		
170					175					180					185		
ATT	GAA	GAG	CCC	ACA	GGT	GAT	GAG	CTA	CCA	ACC	AAG	AAG	GGG	CGG	AGG	626	
Ile	Glu	Glu	Pro	Thr	Gly	Asp	Glu	Leu	Pro	Thr	Lys	Lys	Gly	Arg	Arg		
				190					195					200			
AAC	CGT	TTC	AAG	TGG	GGC	CCA	GCA	TCC	CAG	CAG	ATC	CTG	TTC	CAG	GCC	674	
Asn	Arg	Phe	Lys	Trp	Gly	Pro	Ala	Ser	Gln	Gln	Ile	Leu	Phe	Gln	Ala		
			205					210					215				
TAT	GAG	AGG	CAG	AAG	AAC	CCT	AGC	AAG	GAG	GAG	CGA	GAG	ACG	CTA	GTG	722	
Tyr	Glu	Arg	Gln	Lys	Asn	Pro	Ser	Lys	Glu	Glu	Arg	Glu	Thr	Leu	Val		
	220						225					230					
GAG	GAG	TGC	AAT	AGG	GCG	GAA	TGC	ATC	CAG	AGA	GGG	GTG	TCC	CCA	TCA	770	
Glu	Glu	Cys	Asn	Arg	Ala	Glu	Cys	Ile	Gln	Arg	Gly	Val	Ser	Pro	Ser		
	235					240					245						
CAG	GCA	CAG	GGG	CTG	GGC	TCC	AAC	CTC	GTC	ACG	GAG	GTG	CGT	GTC	TAC	818	
Gln	Ala	Gln	Gly	Leu	Gly	Ser	Asn	Leu	Val	Thr	Glu	Val	Arg	Val	Tyr		
250					255					260					265		
AAC	TGG	TTT	GCC	AAC	CGG	CGC	AAA	GAA	GAA	GCC	TTC	CGG	CAC	AAG	CTG	866	
Asn	Trp	Phe	Ala	Asn	Arg	Arg	Lys	Glu	Glu	Ala	Phe	Arg	His	Lys	Leu		
			270					275						280			
GCC	ATG	GAC	ACG	TAC	AGC	GGG	CCC	CCC	CCA	GGG	CCA	GGC	CCG	GGA	CCT	914	
Ala	Met	Asp	Thr	Tyr	Ser	Gly	Pro	Pro	Pro	Gly	Pro	Gly	Pro	Gly	Pro		
			285				290						295				
GCG	CTG	CCC	GCT	CAC	AGC	TCC	CCT	GGC	CTG	CCT	CCA	CCT	GCC	CTC	TCC	962	
Ala	Leu	Pro	Ala	His	Ser	Ser	Pro	Gly	Leu	Pro	Pro	Pro	Ala	Leu	Ser		
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CCC	AGT	AAG	GTC	CAC	GGT	GTG	CGC	TNT	GGA	CAG	CCT	GCG	ACC	AGT	GAG	1010	
Pro	Ser	Lys	Val	His	Gly	Val	Arg		Gly	Gln	Pro	Ala	Thr	Ser	Glu		
	315					320						325					
ACT	GCA	GAA	GTA	CCC	TCA	AGC	AGC	GGC	GGT	CCC	TTA	GTG	ACA	GTG	TCT	1058	
Thr	Ala	Glu	Val	Pro	Ser	Ser	Ser	Gly	Gly	Pro	Leu	Val	Thr	Val	Ser		
	330					335					340						
ACA	CCC	CTC	CAC	CAA	GTG	TCC	CCC	ACG	GGC	CTG	GAG	CCC	AGC	CAC	AGC	1106	
Thr	Pro	Leu	His	Gln	Val	Ser	Pro	Thr	Gly	Leu	Glu	Pro	Ser	His	Ser		
	345				350					355					360		
CTG	CTG	AGT	ACA	GAA	GCC	AAG	CTG	GTC	TCA	GCA	GCT	GGG	GGC	CCC	CTC	1154	
Leu	Leu	Ser	Thr	Glu	Ala	Lys	Leu	Val	Ser	Ala	Ala	Gly	Gly	Pro	Leu		

365										370					375					
CCC	CCT	GTC	AGC	ACC	CTG	ACA	GCA	CTG	CAC	AGC	TTG	GAG	CAG	ACA	TCC	1202				
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			380						385						390					
CCA	GGC	CTC	AAC	CAG	CAG	CCC	CAG	AAC	CTC	ATC	ATG	GCC	TCA	CTT	CCT	1250				
Pro	Gly	Leu	Asn	Gln	Gln	Pro	Gln	Asn	Leu	Ile	Met	Ala	Ser	Leu	Pro					
			395						400						405					
GGG	GTC	ATG	ACC	ATC	GGG	CCT	GGT	GAG	CCT	GCC	TCC	CTG	GGT	CCT	ACG	1298				
Gly	Val	Met	Thr	Ile	Gly	Pro	Gly	Glu	Pro	Ala	Ser	Leu	Gly	Pro	Thr					
			410						415						420					
TTC	ACC	AAC	ACA	GGT	GCC	TCC	ACC	CTG	GTC	ATC	GGC	CTG	GCC	TCC	ACG	1346				
Phe	Thr	Asn	Thr	Gly	Ala	Ser	Thr	Leu	Val	Ile	Gly	Leu	Ala	Ser	Thr					
			425						430						440					
CAG	GCA	CAG	AGT	GTG	CCG	GTC	ATC	AAC	AGC	ATG	GGC	AGC	AGC	CTG	ACC	1394				
Gln	Ala	Gln	Ser	Val	Pro	Val	Ile	Asn	Ser	Met	Gly	Ser	Ser	Leu	Thr					
			445						450						455					
ACC	CTG	CAG	CCC	GTC	CAG	TTC	TCC	CAG	CCG	CTG	CAC	CCC	TCC	TAC	CAG	1442				
Thr	Leu	Gln	Pro	Val	Gln	Phe	Ser	Gln	Pro	Leu	His	Pro	Ser	Tyr	Gln					
			460						465						470					
CAG	CCG	CTC	ATG	CCA	CCT	GTG	CAG	AGC	CAT	GTG	ACC	CAG	AGC	CCC	TTC	1490				
Gln	Pro	Leu	Met	Pro	Pro	Val	Gln	Ser	His	Val	Thr	Gln	Ser	Pro	Phe					
			475						480						485					
ATG	GCC	ACC	ATG	GCT	CAG	CTG	CAG	AGC	CCC	CAC	GCC	CTC	TAC	AGC	CAC	1538				
Met	Ala	Thr	Met	Ala	Gln	Leu	Gln	Ser	Pro	His	Ala	Leu	Tyr	Ser	His					
			490						495						500					
AAG	CCC	GAG	GTG	GCC	CAG	TAC	ACC	CAC	ACG	GGC	CTG	CTC	CCG	CAG	ACT	1586				
Lys	Pro	Glu	Val	Ala	Gln	Tyr	Thr	His	Thr	Gly	Leu	Leu	Pro	Gln	Thr					
			505						510						520					
ATG	CTC	ATC	ACC	GAC	ACC	ACC	AAC	CTG	AGC	GCC	CTG	GCC	AGC	CTC	ACG	1634				
Met	Leu	Ile	Thr	Asp	Thr	Thr	Asn	Leu	Ser	Ala	Leu	Ala	Ser	Leu	Thr					
			525						530						535					
CCC	ACC	AAG	CAG	GTC	TTC	ACC	TCA	GAC	ACT	GAG	GCC	TCC	AGT	GAG	TCC	1682				
Pro	Thr	Lys	Gln	Val	Phe	Thr	Ser	Asp	Thr	Glu	Ala	Ser	Ser	Glu	Ser					
			540						545						550					
GGG	CTT	CAC	ACG	CCG	GCA	TCT	CAG	GCC	ACC	ACC	CTC	CAC	GTC	CCC	AGC	1730				
Gly	Leu	His	Thr	Pro	Ala	Ser	Gln	Ala	Thr	Thr	Leu	His	Val	Pro	Ser					
			555						560						565					
CAG	GAC	CCT	GCC	GGC	ATC	CAG	CAC	CTG	CAG	CCG	GCC	CAC	CGG	CTC	AGC	1778				
Gln	Asp	Pro	Ala	Gly	Ile	Gln	His	Leu	Gln	Pro	Ala	His	Arg	Leu	Ser					
			570						575						580					
GCC	AGC	CCC	ACA	GTG	TCC	TCC	AGC	AGC	CTG	GTG	CTG	TAC	CAG	AGC	TCA	1826				
Ala	Ser	Pro	Thr	Val	Ser	Ser	Ser	Ser	Leu	Val	Leu	Tyr	Gln	Ser	Ser					
			585						590						600					

GAC TCC AGC AAT GGC CAG AGC CAC CTG CTG CCA TCC AAC CAC AGC GTC	1874
Asp Ser Ser Asn Gly Gln Ser His Leu Leu Pro Ser Asn His Ser Val	
605 610 615	
ATC GAG ACC TTC ATC TCC ACC CAG ATG GCC TCT TCC TCC CAG	1916
Ile Glu Thr Phe Ile Ser Thr Gln Met Ala Ser Ser Ser Gln	
620 625 630	
TAACCACGGC ACCTGGGCCC TGGGGCCTGT ACTGCCTGCT TGGGGGGTGA TGAGGGCAGC	1976
AGCCAGCCCT GCCTGGAGGA CCTGAGCCTG CCGAGCAACC GTGGCCCTTC CTGGACAGCT	2036
GTGCCTCGCT CCCCCTCTG CTCTGATGCA TCAGAAAGGG AGGGCTCTGA GGCGCCCCAA	2096
CCCGTGGAGG CTGCTCGGGG TGCACAGGAG GGGGTCGTGG AGAGCTAGGA GCAAAGCCTG	2156
TTCATGGCAG ATGTAGGAGG GACTGTCGCT GCTTCGTGGG ATACAGTCTT CTTACTTGGA	2216
ACTGAAGGGG GCGGCCTATG ACTTGGGCAC CCCCAGCCTG GGCCTATGGA GAGCCCTGGG	2276
ACCGCTACAC CACTCTGGCA GCCACACTTC TCAGGACACA GGCCTGTGTA GCTGTGACCT	2336
GCTGAGCTCT GAGAGGCCCT GGATCAGCGT GGCCTTGTTT TGTACCAAT GTACCCACCG	2396
GGCCACTCCT TCCTGCCCCA ACTCCTTCCA GCTAGTGACC CACATGCCAT TTGTACTGAC	2456
CCCATCACCT ACTCACACAG GCATTTCTCT GGTGGCTACT CTGTGCCAGA GCCTGGGGCT	2516
CTAACTGCCT GAGCCCAGGG AGGCCGAAGC TAACAGGGAA GGCAGGCAGG GCTCTCCTGG	2576
TCTTCCCATC CCCAGCGATT CCCTCTCCCA GGCCCCATGA CCTCCAGCTT TCCTGTATTT	2636
CTTCCCAAGA GCATGATGCC TCTGAGGCCA GCCTGGCCTC CTGCCTCTAC TGGGAAGGCT	2696
ACTTCGGGGC TGGGAAGTCG TCCTTACTCC TGTGGGAGCC TCGCAACCCG TGCCAAGTCC	2756
AGGTCCTGGT GGGGCAGCTC CTCTGTCTCG AGCGCCCTGC AGACCCTGCC CTTGTTTGGG	2816
GCAGGAGTAG CTGAGCTCAC AAGGCAGCAA GGCCCGAGCA GCTGAGCAGG GCCGGGGAAC	2876
TGGCCAAGCT GAGGTGCCCCA GGAGAAGAAA GAGGTGACCC CAGGGCACAG GAGCTACCTG	2936
TGTGGACAGG ACTAACACTC AGAAGCCTGG GTGCCTGGCT GGCTGAGGGC AGTTCGCAGC	2996
CACCCTGAGG AGTCTGAGGT CCTGAGCACT GCCAGGAGGG ACAAAGGAGC CTGTGAACCC	3056
AGGACAAGCA TGGTCCCACA TCCCTGGGCC TGCTGCTGAG AACCTGGCCT TCAGTGTACC	3116
GCGTCTACCC TGGGATTCAG GAAAAGGCCT GGGGTGACCC GGCACCCCTT GCAGCTTGTA	3176
GCCAGCCGGG GCGAGTGGCA CGTTTATTTA ACTTTTAGTA AAGTCAAGGA GAAATGCGGT	3236
GG	3238
<210> 4	
<211> 630	

<212> PRT

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 4

Met	Val	Ser	Lys	Leu	Ser	Gln	Leu	Gln	Thr	Glu	Leu	Leu	Ala	Ala	Leu	
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Leu	Glu	Ser	Gly	Leu	Ser	Lys	Glu	Ala	Leu	Ile	Gln	Ala	Leu	Gly	Glu	
			20					25					30			
Pro	Gly	Pro	Tyr	Leu	Leu	Ala	Gly	Glu	Gly	Pro	Leu	Asp	Lys	Gly	Glu	
			35				40					45				
Ser	Cys	Gly	Gly	Gly	Arg	Gly	Glu	Leu	Ala	Glu	Leu	Pro	Asn	Gly	Leu	
	50					55					60					
Gly	Glu	Thr	Arg	Gly	Ser	Glu	Asp	Glu	Thr	Asp	Asp	Asp	Gly	Glu	Asp	
65					70					75					80	
Phe	Thr	Pro	Pro	Ile	Leu	Lys	Glu	Leu	Glu	Asn	Leu	Ser	Pro	Glu	Glu	
				85					90						95	
Ala	Ala	His	Gln	Lys	Ala	Val	Val	Glu	Thr	Leu	Leu	Gln	Glu	Asp	Pro	
			100					105					110			
Trp	Arg	Val	Ala	Lys	Met	Val	Lys	Ser	Tyr	Leu	Gln	Gln	His	Asn	Ile	
		115					120					125				
Pro	Gln	Gln	Glu	Val	Val	Asp	Thr	Thr	Gly	Leu	Asn	Gln	Ser	His	Leu	
		130				135					140					
Ser	Gln	His	Leu	Asn	Lys	Gly	Thr	Pro	Met	Lys	Thr	Gln	Lys	Arg	Ala	
145					150					155					160	
Ala	Leu	Tyr	Thr	Trp	Tyr	Val	Arg	Lys	Gln	Arg	Glu	Val	Ala	Gln	Gln	
				165					170					175		
Phe	Thr	His	Ala	Gly	Gln	Gly	Gly	Leu	Ile	Glu	Glu	Pro	Thr	Gly	Asp	
			180					185						190		
Glu	Leu	Pro	Thr	Lys	Lys	Gly	Arg	Arg	Asn	Arg	Phe	Lys	Trp	Gly	Pro	
		195					200					205				
Ala	Ser	Gln	Gln	Ile	Leu	Phe	Gln	Ala	Tyr	Glu	Arg	Gln	Lys	Asn	Pro	
		210				215					220					
Ser	Lys	Glu	Glu	Arg	Glu	Thr	Leu	Val	Glu	Glu	Cys	Asn	Arg	Ala	Glu	
225					230					235					240	
Cys	Ile	Gln	Arg	Gly	Val	Ser	Pro	Ser	Gln	Ala	Gln	Gly	Leu	Gly	Ser	
				245					250					255		
Asn	Leu	Val	Thr	Glu	Val	Arg	Val	Tyr	Asn	Trp	Phe	Ala	Asn	Arg	Arg	
			260					265					270			

Lys Glu Glu Ala Phe Arg His Lys Leu Ala Met Asp Thr Tyr Ser Gly  
 275 280 285  
 Pro Pro Pro Gly Pro Gly Pro Gly Pro Ala Leu Pro Ala His Ser Ser  
 290 295 300  
 Pro Gly Leu Pro Pro Pro Ala Leu Ser Pro Ser Lys Val His Gly Val  
 305 310 315 320  
 Arg Gly Gln Pro Ala Thr Ser Glu Thr Ala Glu Val Pro Ser Ser Ser  
 325 330 335  
 Gly Gly Pro Leu Val Thr Val Ser Thr Pro Leu His Gln Val Ser Pro  
 340 345 350  
 Thr Gly Leu Glu Pro Ser His Ser Leu Leu Ser Thr Glu Ala Lys Leu  
 355 360 365  
 Val Ser Ala Ala Gly Gly Pro Leu Pro Pro Val Ser Thr Leu Thr Ala  
 370 375 380  
 Leu His Ser Leu Glu Gln Thr Ser Pro Gly Leu Asn Gln Gln Pro Gln  
 385 390 395 400  
 Asn Leu Ile Met Ala Ser Leu Pro Gly Val Met Thr Ile Gly Pro Gly  
 405 410 415  
 Glu Pro Ala Ser Leu Gly Pro Thr Phe Thr Asn Thr Gly Ala Ser Thr  
 420 425 430  
 Leu Val Ile Gly Leu Ala Ser Thr Gln Ala Gln Ser Val Pro Val Ile  
 435 440 445  
 Asn Ser Met Gly Ser Ser Leu Thr Thr Leu Gln Pro Val Gln Phe Ser  
 450 455 460  
 Gln Pro Leu His Pro Ser Tyr Gln Gln Pro Leu Met Pro Pro Val Gln  
 465 470 475 480  
 Ser His Val Thr Gln Ser Pro Phe Met Ala Thr Met Ala Gln Leu Gln  
 485 490 495  
 Ser Pro His Ala Leu Tyr Ser His Lys Pro Glu Val Ala Gln Tyr Thr  
 500 505 510  
 His Thr Gly Leu Leu Pro Gln Thr Met Leu Ile Thr Asp Thr Thr Asn  
 515 520 525  
 Leu Ser Ala Leu Ala Ser Leu Thr Pro Thr Lys Gln Val Phe Thr Ser  
 530 535 540  
 Asp Thr Glu Ala Ser Ser Glu Ser Gly Leu His Thr Pro Ala Ser Gln  
 545 550 555 560  
 Ala Thr Thr Leu His Val Pro Ser Gln Asp Pro Ala Gly Ile Gln His  
 565 570 575

Leu Gln Pro Ala His Arg Leu Ser Ala Ser Pro Thr Val Ser Ser Ser  
580 585 590

Ser Leu Val Leu Tyr Gln Ser Ser Asp Ser Ser Asn Gly Gln Ser His  
595 600 605

Leu Leu Pro Ser Asn His Ser Val Ile Glu Thr Phe Ile Ser Thr Gln  
610 615 620

Met Ala Ser Ser Ser Gln  
625 630

<210> 5

<211> 3239

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> CDS

<222> (24)..(965)

<220>

<221> modified\_base

<222> (989)

<223> N = A, C, G, or T

<400> 5

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Met Val Ser Lys Leu Ser Gln Leu Gln  
1 5

ACG GAG CTC CTG GCG GCC CTG CTC GAG TCA GGG CTG AGC AAA GAG GCA 98  
Thr Glu Leu Leu Ala Ala Leu Leu Glu Ser Gly Leu Ser Lys Glu Ala  
10 15 20 25

CTG ATC CAG GCA CTG GGT GAG CCG GGG CCC TAC CTC CTG GCT GGA GAA 146  
Leu Ile Gln Ala Leu Gly Glu Pro Gly Pro Tyr Leu Leu Ala Gly Glu  
30 35 40

GGC CCC CTG GAC AAG GGG GAG TCC TGC GGC GGC GGT CGA GGG GAG CTG 194  
Gly Pro Leu Asp Lys Gly Glu Ser Cys Gly Gly Gly Arg Gly Glu Leu  
45 50 55

GCT GAG CTG CCC AAT GGG CTG GGG GAG ACT CGG GGC TCC GAG GAC GAG 242  
Ala Glu Leu Pro Asn Gly Leu Gly Glu Thr Arg Gly Ser Glu Asp Glu  
60 65 70

ACG GAC GAC GAT GGG GAA GAC TTC ACG CCA CCC ATC CTC AAA GAG CTG 290  
Thr Asp Asp Asp Gly Glu Asp Phe Thr Pro Pro Ile Leu Lys Glu Leu  
75 80 85

GAG AAC CTC AGC CCT GAG GAG GCG GCC CAC CAG AAA GCC GTG GTG GAG 338

Glu Asn Leu Ser Pro Glu Glu Ala Ala His Gln Lys Ala Val Val Glu	
90 95 100 105	
ACC CTT CTG CAG GAG GAC CCG TGG CGT GTG GCG AAG ATG GTC AAG TCC	386
Thr Leu Leu Gln Glu Asp Pro Trp Arg Val Ala Lys Met Val Lys Ser	
110 115 120	
TAC CTG CAG CAG CAC AAC ATC CCA CAG CGG GAG GTG GTC GAT ACC ACT	434
Tyr Leu Gln Gln His Asn Ile Pro Gln Arg Glu Val Val Asp Thr Thr	
125 130 135	
GGC CTC AAC CAG TCC CAC CTG TCC CAA CAC CTC AAC AAG GGC ACT CCC	482
Gly Leu Asn Gln Ser His Leu Ser Gln His Leu Asn Lys Gly Thr Pro	
140 145 150	
ATG AAG ACG CAG AAG CGG GCC GCC CTG TAC ACC TGG TAC GTC CGC AAG	530
Met Lys Thr Gln Lys Arg Ala Ala Leu Tyr Thr Trp Tyr Val Arg Lys	
155 160 165	
CAG CGA GAG GTG GCG CAG CAG TTC ACC CAT GCA GGG CAG GGA GGG CTG	578
Gln Arg Glu Val Ala Gln Gln Phe Thr His Ala Gly Gln Gly Gly Leu	
170 175 180 185	
ATT GAA GAG CCC ACA GGT GAT GAG CTA CCA ACC AAG AAG GGG CGG AGG	626
Ile Glu Glu Pro Thr Gly Asp Glu Leu Pro Thr Lys Lys Gly Arg Arg	
190 195 200	
AAC CGT TTC AAG TGG GGC CCA GCA TCC CAG CAG ATC CTG TTC CAG GCC	674
Asn Arg Phe Lys Trp Gly Pro Ala Ser Gln Gln Ile Leu Phe Gln Ala	
205 210 215	
TAT GAG AGG CAG AAG AAC CCT AGC AAG GAG GAG CGA GAG ACG CTA GTG	722
Tyr Glu Arg Gln Lys Asn Pro Ser Lys Glu Glu Arg Glu Thr Leu Val	
220 225 230	
GAG GAG TGC AAT AGG GCG GAA TGC ATC CAG AGA GGG GTG TCC CCA TCA	770
Glu Glu Cys Asn Arg Ala Glu Cys Ile Gln Arg Gly Val Ser Pro Ser	
235 240 245	
CAG GCA CAG GGG CTG GGC TCC AAC CTC GTC ACG GAG GTG CGT GTC TAC	818
Gln Ala Gln Gly Leu Gly Ser Asn Leu Val Thr Glu Val Arg Val Tyr	
250 255 260 265	
AAC TGG TTT GCC AAC CGG CGC AAA GAA GAA GCC TTC CGG CAC AAG CTG	866
Asn Trp Phe Ala Asn Arg Arg Lys Glu Glu Ala Phe Arg His Lys Leu	
270 275 280	
GCC ATG GAC ACG TAC AGC GGG CCC CCC CCC AGG GCC AGG CCC GGG ACC	914
Ala Met Asp Thr Tyr Ser Gly Pro Pro Pro Arg Ala Arg Pro Gly Thr	
285 290 295	
TGC GCT GCC CGC TCA CAG CTC CCC TGG CCT GCC TCC ACC TGC CCT CTC	962
Cys Ala Ala Arg Ser Gln Leu Pro Trp Pro Ala Ser Thr Cys Pro Leu	
300 305 310	
CCC CAGTAAGGTC CACGGTGTGC GCTNTGGACA GCCTGCGACC AGTGAGACTG	1015
Pro	

CAGAAGTACC	CTCAAGCAGC	GGCGGTCCCT	TAGTGACAGT	GTCTACACCC	CTCCACCAAG	1075
TGTCCCCCAC	GGGCCTGGAG	CCCAGCCACA	GCCTGCTGAG	TACAGAAGCC	AAGCTGGTCT	1135
CAGCAGCTGG	GGGCCCCCTC	CCCCCTGTCA	GCACCCTGAC	AGCACTGCAC	AGCTTGGAGC	1195
AGACATCCCC	AGGCCTCAAC	CAGCAGCCCC	AGAACCTCAT	CATGGCCTCA	CTTCCTGGGG	1255
TCATGACCAT	CGGGCCTGGT	GAGCCTGCCT	CCCTGGGTCC	TACGTTACAC	AACACAGGTG	1315
CCTCCACCCT	GGTCATCGGC	CTGGCCTCCA	CGCAGGCACA	GAGTGTGCCG	GTCATCAACA	1375
GCATGGGCAG	CAGCCTGACC	ACCCTGCAGC	CCGTCCAGTT	CTCCCAGCCG	CTGCACCCCT	1435
CCTACCAGCA	GCCGCTCATG	CCACCTGTGC	AGAGCCATGT	GACCCAGAGC	CCCTTCATGG	1495
CCACCATGGC	TCAGCTGCAG	AGCCCCACG	CCCTCTACAG	CCACAAGCCC	GAGGTGGCCC	1555
AGTACACCCA	CACGGGCCTG	CTCCCGCAGA	CTATGCTCAT	CACCGACACC	ACCAACCTGA	1615
GCGCCCTGGC	CAGCCTCACG	CCCACCAAGC	AGGTCTTCAC	CTCAGACACT	GAGGCCTCCA	1675
GTGAGTCCGG	GCTTCACACG	CCGGCATCTC	AGGCCACCAC	CCTCCACGTC	CCCAGCCAGG	1735
ACCCTGCCGG	CATCCAGCAC	CTGCAGCCGG	CCCACCGGCT	CAGCGCCAGC	CCCACAGTGT	1795
CCTCCAGCAG	CCTGGTGCTG	TACCAGAGCT	CAGACTCCAG	CAATGGCCAG	AGCCACCTGC	1855
TGCCATCCAA	CCACAGCGTC	ATCGAGACCT	TCATCTCCAC	CCAGATGGCC	TCTTCCTCCC	1915
AGTAACCACG	GCACCTGGGC	CCTGGGGCCT	GTA CTGCCTG	CTTGGGGGGT	GATGAGGGCA	1975
GCAGCCAGCC	CTGCCTGGAG	GACCTGAGCC	TGCCGAGCAA	CCGTGGCCCT	TCCTGGACAG	2035
CTGTGCCTCG	CTCCCCACTC	TGCTCTGATG	CATCAGAAAG	GGAGGGCTCT	GAGGCGCCCC	2095
AACCCGTGGA	GGCTGCTCGG	GGTGCACAGG	AGGGGGTCGT	GGAGAGCTAG	GAGCAAAGCC	2155
TGTTTCATGGC	AGATGTAGGA	GGGACTGTCTG	CTGCTTCGTG	GGATACAGTC	TTCTTACTTG	2215
GAAGTGAAGG	GGGCGGCCCTA	TGACTTGGGC	ACCCCAGCC	TGGGCCTATG	GAGAGCCCTG	2275
GGACCGCTAC	ACCAC TCTGG	CAGCCACACT	TCTCAGGACA	CAGGCCTGTG	TAGCTGTGAC	2335
CTGCTGAGCT	CTGAGAGGCC	CTGGATCAGC	GTGGCCTTGT	TCTGTCACCA	ATGTACCCAC	2395
CGGGCCACTC	CTTCCTGCCC	CAACTCCTTC	CAGCTAGTGA	CCCACATGCC	ATTTGTACTG	2455
ACCCCATCAC	CTACTCACAC	AGGCATTTCC	TGGGTGGCTA	CTCTGTGCCA	GAGCCTGGGG	2515
CTCTAACTGC	CTGAGCCCAG	GGAGGCCGAA	GCTAACAGGG	AAGGCAGGCA	GGGCTCTCCT	2575
GGTCTTCCCA	TCCCCAGCGA	TTCCCTCTCC	CAGGCCCCAT	GACCTCCAGC	TTTCCTGTAT	2635
TTCTTCCCAA	GAGCATGATG	CCTCTGAGGC	CAGCCTGGCC	TCCTGCCTCT	ACTGGGAAGG	2695



CTACTTCGGG GCTGGGAAGT CGTCCTTACT CCTGTGGGAG CCTCGCAACC CGTGCCAAGT 2755  
 CCAGGTCCTG GTGGGGCAGC TCCTCTGTCT CGAGCGCCCT GCAGACCCTG CCCTTGTTTG 2815  
 GGGCAGGAGT AGCTGAGCTC ACAAGGCAGC AAGGCCCCGAG CAGCTGAGCA GGGCCGGGGA 2875  
 ACTGGCCAAG CTGAGGTGCC CAGGAGAAGA AAGAGGTGAC CCCAGGGCAC AGGAGCTACC 2935  
 TGTGTGGACA GGAATAACAC TCAGAAGCCT GGGTGCCTGG CTGGCTGAGG GCAGTTCGCA 2995  
 GCCACCCTGA GGAGTCTGAG GTCCTGAGCA CTGCCAGGAG GGACAAAGGA GCCTGTGAAC 3055  
 CCAGGACAAG CATGGTCCCA CATCCCTGGG CCTGCTGCTG AGAACCTGGC CTTCACTGTA 3115  
 CCGCGTCTAC CCTGGGATTC AGGAAAAGGC CTGGGGTGAC CCGGCACCCC CTGCAGCTTG 3175  
 TAGCCAGCCG GGGCGAGTGG CACGTTTATT TAACTTTTAG TAAAGTCAAG GAGAAATGCG 3235  
 GTGA 3239

<210> 6

<211> 314

<212> PRT

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
 Peptide

<400> 6

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Leu	Glu	Ser	Gly	Leu	Ser	Lys	Glu	Ala	Leu	Ile	Gln	Ala	Leu	Gly	Glu
			20				25						30		
Pro	Gly	Pro	Tyr	Leu	Leu	Ala	Gly	Glu	Gly	Pro	Leu	Asp	Lys	Gly	Glu
			35				40					45			
Ser	Cys	Gly	Gly	Gly	Arg	Gly	Glu	Leu	Ala	Glu	Leu	Pro	Asn	Gly	Leu
	50					55					60				
Gly	Glu	Thr	Arg	Gly	Ser	Glu	Asp	Glu	Thr	Asp	Asp	Asp	Gly	Glu	Asp
	65				70				75					80	
Phe	Thr	Pro	Pro	Ile	Leu	Lys	Glu	Leu	Glu	Asn	Leu	Ser	Pro	Glu	Glu
				85				90						95	
Ala	Ala	His	Gln	Lys	Ala	Val	Val	Glu	Thr	Leu	Leu	Gln	Glu	Asp	Pro
			100					105					110		
Trp	Arg	Val	Ala	Lys	Met	Val	Lys	Ser	Tyr	Leu	Gln	Gln	His	Asn	Ile
		115					120					125			
Pro	Gln	Arg	Glu	Val	Val	Asp	Thr	Thr	Gly	Leu	Asn	Gln	Ser	His	Leu
	130					135					140				

Ser Gln His Leu Asn Lys Gly Thr Pro Met Lys Thr Gln Lys Arg Ala  
 145 150 155 160  
 Ala Leu Tyr Thr Trp Tyr Val Arg Lys Gln Arg Glu Val Ala Gln Gln  
 165 170 175  
 Phe Thr His Ala Gly Gln Gly Gly Leu Ile Glu Glu Pro Thr Gly Asp  
 180 185 190  
 Glu Leu Pro Thr Lys Lys Gly Arg Arg Asn Arg Phe Lys Trp Gly Pro  
 195 200 205  
 Ala Ser Gln Gln Ile Leu Phe Gln Ala Tyr Glu Arg Gln Lys Asn Pro  
 210 215 220  
 Ser Lys Glu Glu Arg Glu Thr Leu Val Glu Glu Cys Asn Arg Ala Glu  
 225 230 235 240  
 Cys Ile Gln Arg Gly Val Ser Pro Ser Gln Ala Gln Gly Leu Gly Ser  
 245 250 255  
 Asn Leu Val Thr Glu Val Arg Val Tyr Asn Trp Phe Ala Asn Arg Arg  
 260 265 270  
 Lys Glu Glu Ala Phe Arg His Lys Leu Ala Met Asp Thr Tyr Ser Gly  
 275 280 285  
 Pro Pro Pro Arg Ala Arg Pro Gly Thr Cys Ala Ala Arg Ser Gln Leu  
 290 295 300  
 Pro Trp Pro Ala Ser Thr Cys Pro Leu Pro  
 305 310

<210> 7  
 <211> 3236  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<220>  
 <221> CDS  
 <222> (24) .. (986)

<220>  
 <221> CDS  
 <222> (990) .. (1271)

<220>  
 <221> modified\_base  
 <222> (988)  
 <223> N = A, C, G, or T

<400> 7

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Met Val Ser Lys Leu Ser Gln Leu Gln	
1 5	
ACG GAG CTC CTG GCG GCC CTG CTC GAG TCA GGG CTG AGC AAA GAG GCA	98
Thr Glu Leu Leu Ala Ala Leu Leu Glu Ser Gly Leu Ser Lys Glu Ala	
10 15 20 25	
CTG ATC CAG GCA CTG GGT GAG CCG GGG CCC TAC CTC CTG GCT GGA GAA	146
Leu Ile Gln Ala Leu Gly Glu Pro Gly Pro Tyr Leu Leu Ala Gly Glu	
30 35 40	
GGC CCC CTG GAC AAG GGG GAG TCC TGC GGC GGC GGT CGA GGG GAG CTG	194
Gly Pro Leu Asp Lys Gly Glu Ser Cys Gly Gly Gly Arg Gly Glu Leu	
45 50 55	
GCT GAG CTG CCC AAT GGG CTG GGG GAG ACT CGG GGC TCC GAG GAC GAG	242
Ala Glu Leu Pro Asn Gly Leu Gly Glu Thr Arg Gly Ser Glu Asp Glu	
60 65 70	
ACG GAC GAC GAT GGG GAA GAC TTC ACG CCA CCC ATC CTC AAA GAG CTG	290
Thr Asp Asp Asp Gly Glu Asp Phe Thr Pro Pro Ile Leu Lys Glu Leu	
75 80 85	
GAG AAC CTC AGC CCT GAG GAG GCG GCC CAC CAG AAA GCC GTG GTG GAG	338
Glu Asn Leu Ser Pro Glu Glu Ala Ala His Gln Lys Ala Val Val Glu	
90 95 100 105	
ACC CTT CTG CAG GAG GAC CCG TGG CGT GTG GCG AAG ATG GTC AAG TCC	386
Thr Leu Leu Gln Glu Asp Pro Trp Arg Val Ala Lys Met Val Lys Ser	
110 115 120	
TAC CTG CAG CAG CAC AAC ATC CCA CAG CGG GAG GTG GTC GAT ACC ACT	434
Tyr Leu Gln Gln His Asn Ile Pro Gln Arg Glu Val Val Asp Thr Thr	
125 130 135	
GGC CTC AAC CAG TCC CAC CTG TCC CAA CAC CTC AAC AAG GGC ACT CCC	482
Gly Leu Asn Gln Ser His Leu Ser Gln His Leu Asn Lys Gly Thr Pro	
140 145 150	
ATG AAG ACG CAG AAG CGG GCC GCC CTG TAC ACC TGG TAC GTC CGC AAG	530
Met Lys Thr Gln Lys Arg Ala Ala Leu Tyr Thr Trp Tyr Val Arg Lys	
155 160 165	
CAG CGA GAG GTG GCG CAG CAG TTC ACC CAT GCA GGG CAG GGA GGG CTG	578
Gln Arg Glu Val Ala Gln Gln Phe Thr His Ala Gly Gln Gly Gly Leu	
170 175 180 185	
ATT GAA GAG CCC ACA GGT GAT GAG CTA CCA ACC AAG AAG GGG CGG AGG	626
Ile Glu Glu Pro Thr Gly Asp Glu Leu Pro Thr Lys Lys Gly Arg Arg	
190 195 200	
AAC CGT TTC AAG TGG GGC CCA GCA TCC CAG CAG ATC CTG TTC CAG GCC	674
Asn Arg Phe Lys Trp Gly Pro Ala Ser Gln Gln Ile Leu Phe Gln Ala	
205 210 215	
TAT GAG AGG CAG AAG AAC CCT AGC AAG GAG GAG CGA GAG ACG CTA GTG	722

Tyr	Glu	Arg	Gln	Lys	Asn	Pro	Ser	Lys	Glu	Glu	Arg	Glu	Thr	Leu	Val		
		220					225					230					
GAG	GAG	TGC	AAT	AGG	GCG	GAA	TGC	ATC	CAG	AGA	GGG	GTG	TCC	CCA	TCA	770	
Glu	Glu	Cys	Asn	Arg	Ala	Glu	Cys	Ile	Gln	Arg	Gly	Val	Ser	Pro	Ser		
		235				240					245						
CAG	GCA	CAG	GGG	CTG	GGC	TCC	AAC	CTC	GTC	ACG	GAG	GTG	CGT	GTC	TAC	818	
Gln	Ala	Gln	Gly	Leu	Gly	Ser	Asn	Leu	Val	Thr	Glu	Val	Arg	Val	Tyr		
		250			255					260					265		
AAC	TGG	TTT	GCC	AAC	CGG	CGC	AAA	GAA	GAA	GCC	TTC	CGG	CAC	AAG	CTG	866	
Asn	Trp	Phe	Ala	Asn	Arg	Arg	Lys	Glu	Glu	Ala	Phe	Arg	His	Lys	Leu		
				270					275					280			
GCC	ATG	GAC	ACG	TAC	AGC	GGG	CCC	CCC	CCA	GGG	CCA	GGC	CCG	GGA	CCT	914	
Ala	Met	Asp	Thr	Tyr	Ser	Gly	Pro	Pro	Pro	Gly	Pro	Gly	Pro	Gly	Pro		
			285					290					295				
GCG	CTG	CCC	GCT	CAC	AGC	TCC	CCT	GGC	CTG	CCT	CCA	CCT	GCC	CTC	TCC	962	
Ala	Leu	Pro	Ala	His	Ser	Ser	Pro	Gly	Leu	Pro	Pro	Pro	Ala	Leu	Ser		
		300					305					310					
CCC	AGT	AAG	GTC	CAC	GGT	GTG	CGC	TNT	GGA	CAG	CCT	GCG	ACC	AGT	GAG	1010	
Pro	Ser	Lys	Val	His	Gly	Val	Arg		Gly	Gln	Pro	Ala	Thr	Ser	Glu		
		315				320						325					
ACT	GCA	GAA	GTA	CCC	TCA	AGC	AGC	GGC	GGT	CCC	TTA	GTG	ACA	GTG	TCT	1058	
Thr	Ala	Glu	Val	Pro	Ser	Ser	Ser	Gly	Gly	Pro	Leu	Val	Thr	Val	Ser		
		330				335					340						
ACA	CCC	CTC	CAC	CAA	GTG	TCC	CCC	ACG	GGC	CTG	GAG	CCC	AGC	CAC	AGC	1106	
Thr	Pro	Leu	His	Gln	Val	Ser	Pro	Thr	Gly	Leu	Glu	Pro	Ser	His	Ser		
		345			350					355					360		
CTG	CTG	AGT	ACA	GAA	GCC	AAG	CTG	GTC	TCA	GCA	GCT	GGG	GGC	CCC	CTC	1154	
Leu	Leu	Ser	Thr	Glu	Ala	Lys	Leu	Val	Ser	Ala	Ala	Gly	Gly	Pro	Leu		
				365				370						375			
CCC	CGT	CAG	CAC	CCT	GAC	AGC	ACT	GCA	CAG	CTT	GGA	GCA	GAC	ATC	CCC	1202	
Pro	Arg	Gln	His	Pro	Asp	Ser	Thr	Ala	Gln	Leu	Gly	Ala	Asp	Ile	Pro		
			380					385					390				
AGG	CCT	CAA	CCA	GCA	GCC	CCA	GAA	CCT	CAT	CAT	GGC	CTC	ACT	TCC	TGG	1250	
Arg	Pro	Gln	Pro	Ala	Ala	Pro	Glu	Pro	His	His	Gly	Leu	Thr	Ser	Trp		
		395				400						405					
GGT	CAT	GAC	CAT	CGG	GCC	TGG	TGAGCCTGCC	TCCCTGGGTC	CTACGTTTAC							1301	
Gly	His	Asp	His	Arg	Ala	Trp											
		410			415												
CAACACAGGT	GCCTCCACCC	TGGTCATCGG	CCTGGCCTCC	ACGCAGGCAC	AGAGTGTGCC											1361	
GGTCATCAAC	AGCATGGGCA	GCAGCCTGAC	CACCCTGCAG	CCCGTCCAGT	TCTCCAGCC											1421	
GCTGCACCCC	TCCTACCAGC	AGCCGCTCAT	GCCACCTGTG	CAGAGCCATG	TGACCCAGAG											1481	

CCCCTTCATG	GCCACCATGG	CTCAGCTGCA	GAGCCCCAC	GCCCTCTACA	GCCACAAGCC	1541
CGAGGTGGCC	CAGTACACCC	ACACGGGCCT	GCTCCCGCAG	ACTATGCTCA	TCACCGACAC	1601
CACCAACCTG	AGCGCCCTGG	CCAGCCTCAC	GCCCACCAAG	CAGGTCTTCA	CCTCAGACAC	1661
TGAGGCCTCC	AGTGAGTCCG	GGCTTCACAC	GCCGGCATCT	CAGGCCACCA	CCCTCCACGT	1721
CCCCAGCCAG	GACCCTGCCG	GCATCCAGCA	CCTGCAGCCG	GCCCACCGGC	TCAGCGCCAG	1781
CCCCACAGTG	TCCTCCAGCA	GCCTGGTGCT	GTACCAGAGC	TCAGACTCCA	GCAATGGCCA	1841
GAGCCACCTG	CTGCCATCCA	ACCACAGCGT	CATCGAGACC	TTCATCTCCA	CCCAGATGGC	1901
CTCTTCCTCC	CAGTAACCAC	GGCACCTGGG	CCCTGGGGCC	TGTA CTGCCT	GCTTGGGGGG	1961
TGATGAGGGC	AGCAGCCAGC	CCTGCCTGGA	GGACCTGAGC	CTGCCGAGCA	ACCGTGGCCC	2021
TTCCTGGACA	GCTGTGCCTC	GCTCCCCACT	CTGCTCTGAT	GCATCAGAAA	GGGAGGGCTC	2081
TGAGGCGCCC	CAACCCGTGG	AGGCTGCTCG	GGGTGCACAG	GAGGGGGTCG	TGGAGAGCTA	2141
GGAGCAAAGC	CTGTTTCATG	CAGATGTAGG	AGGGACTGTC	GCTGCTTCGT	GGGATACAGT	2201
CTTCTTACTT	GGA ACTGAAG	GGGGCGGCCT	ATGACTTGGG	CACCCCCAGC	CTGGGCCTAT	2261
GGAGAGCCCT	GGGACCGCTA	CACCACTCTG	GCAGCCACAC	TTCTCAGGAC	ACAGGCCTGT	2321
G TAGCTGTGA	CCTGCTGAGC	TCTGAGAGGC	CCTGGATCAG	CGTGGCCTTG	TTCTGTCACC	2381
AATGTACCCA	CCGGGCCACT	CCTTCCTGCC	CCAACTCCTT	CCAGCTAGTG	ACCCACATGC	2441
CATTTGTACT	GACCCCATCA	CCTACTCACA	CAGGCATTTT	CTGGGTGGCT	ACTCTGTGCC	2501
AGAGCCTGGG	GCTCTAACTG	CCTGAGCCCA	GGGAGGCCGA	AGCTAACAGG	GAAGGCAGGC	2561
AGGGCTCTCC	TGGTCTTCCC	ATCCCCAGCG	ATTCCCTCTC	CCAGGCCCCA	TGACCTCCAG	2621
CTTTCCTGTA	TTTCTTCCCA	AGAGCATGAT	GCCTCTGAGG	CCAGCCTGGC	CTCCTGCCTC	2681
TACTGGGAAG	GCTACTTCGG	GGCTGGGAAG	TCGTCTTAC	TCCTGTGGGA	GCCTCGCAAC	2741
CCGTGCCAAG	TCCAGGTCCT	GGTGGGGCAG	CTCCTCTGTC	TCGAGCGCCC	TGCAGACCCT	2801
GCCCTTGTTT	GGGGCAGGAG	TAGCTGAGCT	CACAAGGCAG	CAAGGCCCCG	GCAGCTGAGC	2861
AGGGCCGGGG	AACTGGCCAA	GCTGAGGTGC	CCAGGAGAAG	AAAGAGGTGA	CCCCAGGGCA	2921
CAGGAGCTAC	CTGTGTGGAC	AGGACTAACA	CTCAGAAGCC	TGGGTGCCTG	GCTGGCTGAG	2981
GGCAGTTCGC	AGCCACCCTG	AGGAGTCTGA	GGTCCTGAGC	ACTGCCAGGA	GGGACAAAGG	3041
AGCCTGTGAA	CCCAGGACAA	GCATGGTCCC	ACATCCCTGG	GCCTGCTGCT	GAGAACCTGG	3101
CCTTCAGTGT	ACCGCGTCTA	CCCTGGGATT	CAGGAAAAGG	CCTGGGGTGA	CCGGGCACCC	3161
CCTGCAGCTT	G TAGCCAGCC	GGGGCGAGTG	GCACGTTTAT	TTAACTTTTA	GTAAAGTCAA	3221

GGAGAAATGC GGTGG

3236

<210> 8

<211> 415

<212> PRT

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<200>

<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 8

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Leu	Glu	Ser	Gly	Leu	Ser	Lys	Glu	Ala	Leu	Ile	Gln	Ala	Leu	Gly	Glu	
			20					25					30			
Pro	Gly	Pro	Tyr	Leu	Leu	Ala	Gly	Glu	Gly	Pro	Leu	Asp	Lys	Gly	Glu	
			35				40					45				
Ser	Cys	Gly	Gly	Gly	Arg	Gly	Glu	Leu	Ala	Glu	Leu	Pro	Asn	Gly	Leu	
	50					55					60					
Gly	Glu	Thr	Arg	Gly	Ser	Glu	Asp	Glu	Thr	Asp	Asp	Asp	Gly	Glu	Asp	
65					70					75					80	
Phe	Thr	Pro	Pro	Ile	Leu	Lys	Glu	Leu	Glu	Asn	Leu	Ser	Pro	Glu	Glu	
				85					90					95		
Ala	Ala	His	Gln	Lys	Ala	Val	Val	Glu	Thr	Leu	Leu	Gln	Glu	Asp	Pro	
			100					105					110			
Trp	Arg	Val	Ala	Lys	Met	Val	Lys	Ser	Tyr	Leu	Gln	Gln	His	Asn	Ile	
		115					120					125				
Pro	Gln	Arg	Glu	Val	Val	Asp	Thr	Thr	Gly	Leu	Asn	Gln	Ser	His	Leu	
		130				135					140					
Ser	Gln	His	Leu	Asn	Lys	Gly	Thr	Pro	Met	Lys	Thr	Gln	Lys	Arg	Ala	
145					150					155					160	
Ala	Leu	Tyr	Thr	Trp	Tyr	Val	Arg	Lys	Gln	Arg	Glu	Val	Ala	Gln	Gln	
				165					170					175		
Phe	Thr	His	Ala	Gly	Gln	Gly	Gly	Leu	Ile	Glu	Glu	Pro	Thr	Gly	Asp	
			180					185					190			
Glu	Leu	Pro	Thr	Lys	Lys	Gly	Arg	Arg	Asn	Arg	Phe	Lys	Trp	Gly	Pro	
		195					200					205				
Ala	Ser	Gln	Gln	Ile	Leu	Phe	Gln	Ala	Tyr	Glu	Arg	Gln	Lys	Asn	Pro	
		210				215					220					
Ser	Lys	Glu	Glu	Arg	Glu	Thr	Leu	Val	Glu	Glu	Cys	Asn	Arg	Ala	Glu	
225					230					235					240	

Cys Ile Gln Arg Gly Val Ser Pro Ser Gln Ala Gln Gly Leu Gly Ser  
                     245                    250                    255  
 Asn Leu Val Thr Glu Val Arg Val Tyr Asn Trp Phe Ala Asn Arg Arg  
                     260                    265                    270  
 Lys Glu Glu Ala Phe Arg His Lys Leu Ala Met Asp Thr Tyr Ser Gly  
                     275                    280                    285  
 Pro Pro Pro Gly Pro Gly Pro Gly Pro Ala Leu Pro Ala His Ser Ser  
                     290                    295                    300  
 Pro Gly Leu Pro Pro Pro Ala Leu Ser Pro Ser Lys Val His Gly Val  
                     305                    310                    315                    320  
 Arg Gly Gln Pro Ala Thr Ser Glu Thr Ala Glu Val Pro Ser Ser Ser  
                     325                    330                    335  
 Gly Gly Pro Leu Val Thr Val Ser Thr Pro Leu His Gln Val Ser Pro  
                     340                    345                    350  
 Thr Gly Leu Glu Pro Ser His Ser Leu Leu Ser Thr Glu Ala Lys Leu  
                     355                    360                    365  
 Val Ser Ala Ala Gly Gly Pro Leu Pro Arg Gln His Pro Asp Ser Thr  
                     370                    375                    380  
 Ala Gln Leu Gly Ala Asp Ile Pro Arg Pro Gln Pro Ala Ala Pro Glu  
                     385                    390                    395                    400  
 Pro His His Gly Leu Thr Ser Trp Gly His Asp His Arg Ala Trp  
                     405                    410                    415

<210> 9  
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           Primer

<221> modified\_base  
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 <223> N = A, C, G, or T

<400> 9  
 GTTAATNATT ACC

13

<210> 10  
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           Primer

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<210> 11 <211> 24 <212> DNA <213> Artificial Sequence <200> <223> Description of Artificial Sequence: Synthetic Primer	
<400> 11 CGGTGGGTAC ATTGGTGACA GAAC	24
<210> 12 <211> 21 <212> DNA <213> Artificial Sequence <200> <223> Description of Artificial Sequence: Synthetic Primer	
<400> 12 GGCAGGCAAA CGCAACCCAC G	21
<210> 13 <211> 21 <212> DNA <213> Artificial Sequence <200> <223> Description of Artificial Sequence: Synthetic Primer	
<400> 13 GAAGGGGGGC TCGTTAGGAG C	21
<210> 14 <211> 21 <212> DNA <213> Artificial Sequence <200> <223> Description of Artificial Sequence: Synthetic Primer	
<400> 14 CATGCACAGT CCCCACCCTC A	21
<210> 15 <211> 21 <212> DNA <213> Artificial Sequence <200> <223> Description of Artificial Sequence: Synthetic Primer	



<400> 15  
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<210> 16  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
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 Primer

<400> 16  
 GGGCAAGGTC AGGGGAATGG A 21

<210> 17  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
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 Primer

<400> 17  
 CAGCCCAGAC CAAACCAGCA C 21

<210> 18  
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 Primer

<400> 18  
 CAGAACCCTC CCCTTCATGC C 21

<210> 19  
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 <200>  
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<400> 19  
 GGTGACTGCT GTCAATGGGA C 21

<210> 20  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
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<400> 20  
 GGCAGACAGG CAGATGGCCT A 21

<210> 21  
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 <212> DNA  
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 Primer

<400> 21  
 GCCTCCCTAG GGACTGCTCC A 21

<210> 22  
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 Primer

<400> 22  
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<210> 23  
 <211> 21  
 <212> DNA  
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 Primer

<400> 23  
 GTTGCCCCAT GAGCCTCCCA C 21

<210> 24  
 <211> 21  
 <212> DNA  
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 Primer

<400> 24  
 GGTCTTGGGC AGGGGTGGGA T 21

<210> 25  
 <211> 21  
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# Primer

<400> 25  
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<210> 26  
<211> 21  
<212> DNA  
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Primer

<400> 26  
CCCCTGCATC CATTGACAGC C 21

<210> 27  
<211> 21  
<212> DNA  
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Primer

<400> 27  
GAGGCCTGGG ACTAGGGCTG T 21

<210> 28  
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Primer

<400> 28  
CTCTGTCACA GGCCGAGGGA G 21

<210> 29  
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Primer

<400> 29  
CCTGTGACAG AGCCCCTCAC C 21

<210> 30  
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Primer

<400> 30  
CGGACAGCAA CAGAAGGGGT G 21

<210> 31  
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Primer

<400> 31  
CAGAGCCCCT CACCCCCACA T 21

<210> 32  
<211> 21  
<212> DNA  
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<400> 32  
GTACCCCTAG GGACAGGCAG G 21

<210> 33  
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Primer

<400> 33  
ACCCCCAAG CAGGCAGTAC A 21

<210> 34  
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<212> DNA  
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<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<221> CDS  
<222> (104)..(217)

<400> 34  
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CGCCCAGGGT AGGGCAGGTG GCCGCGGCGT GGAGGCAGGG AGA ATG CGA CTC TCC 115  
Met Arg Leu Ser

AAA ACC CTC GTC GAC ATG GAC ATG GCC GAC TAC AGT GCT GCA CTG GAC 163  
 Lys Thr Leu Val Asp Met Asp Met Ala Asp Tyr Ser Ala Ala Leu Asp  
     5                    10                    15                    20

CCA GCC TAC ACC ACC CTG GAA TTT GAG AAT GTG CAG GTG TTG ACG ATG 211  
 Pro Ala Tyr Thr Thr Leu Glu Phe Glu Asn Val Gln Val Leu Thr Met  
                     25                    30                    35

GGC AAT GGTAGGTGGG GGCAGATGTG CCCAGGTGTG CCAGTGGGGG CAGGTGTGCC 267  
 Gly Asn

TGGGTCCAGG AGCAGATCTT TGGCACTCAA CTTTGGGGTG GGAGGAGAAT GATACAAAAT 327

GGTAGGTTGG TCCTACAGGC CAGCACAGGT GTTGCCAAGT GAAGCCCATG TGCCCAGGCA 387

CAGTGATCAC AGGCATTCTG GGTGAAGGGA GGCCTGCAAG GGCCAATTTT CAGCAAAAGT 447

CGATCCCGGC TATTCCTCCC AGGCCCTTCC AGTCCTCACT GCCTCACAGT GGCTCTGCTT 507

GGCGCTTGGC ACAGTGACAT GATGGTGAGC TCCCCCTTGG TGCCCAGCTC CAGCGATTCA 567

GCCCAGCACG GCCCCTTCGT GAACCCCTTG GGCCTAGGTT CAGAGAGACG GCAAGGGATG 627

TTGTATCCCT GGAGATGGTG GTTGGAGACA TAACCGCATT TCTC 671

<210> 35

<211> 38

<212> PRT

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
 Peptide

<400> 35

Met Arg Leu Ser Lys Thr Leu Val Asp Met Asp Met Ala Asp Tyr Ser  
     1                    5                    10                    15

Ala Ala Leu Asp Pro Ala Tyr Thr Thr Leu Glu Phe Glu Asn Val Gln  
                     20                    25                    30

Val Leu Thr Met Gly Asn  
                     35

<210> 36

<211> 796

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
 Primer

<220>

<221> CDS

<222> (286) .. (312)

<220>

<221> CDS

<222> (316) .. (375)

<400> 36

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GGACCTGTTG GAGTGCCCTG TTCTTCCTGC ATCTTTATCC TGTATGGGCG TTTTGTCTGT 120

TGCCCCATATT TGTACCTGCT GTGTATATAT GCAGTTCCCT GTGCTGCGGG CGGGGGTCAG 180

CGGTCTCTGG TGTGCACGAC TGCACAGACC CAAATGCAGG ACTCTGTTGT TGCCACTCAC 240

CAAGTGAGAT TCATATCAGC AACATGTCCG TTTGTCTCTG AGCAG ATT TGT TGC 294  
Ile Cys Cys  
1

CGC TGC GTC TCG CCA GAT TGA GGC ATC CCC TCC GAC ATC ACT GGA GCA 342  
Arg Cys Val Ser Pro Asp Gly Ile Pro Ser Asp Ile Thr Gly Ala  
5 10 15

TAT CTG GAG GGG TGG ACA GTT CTC CAC AGG GAG GTAGGGGAAA AGAGGAGGCC 395  
Tyr Leu Glu Gly Trp Thr Val Leu His Arg Glu  
20 25

CGGAAACCCC TCCTGGAGGG AAGAGCCCCA TCGGTCCCAG GCCAGCCTCA GAGGAGAGGG 455

GGCAGGCAGC TGGCTGAGGT CAGCCTGCCA CCCTGCTTCC TTCTGTGTCT TGGAGCCACT 515

CAGCCAGTAT GAGGCTGCAG CTCCAGCTGA GGTCTGGAAT CTTGTGGTCA GCTCAGCTAG 575

GGTGAGGAGG CAGCTGCTGG GCACTGCTTG TTGTCAGCTC AGCAGGTGCT CACCTGCCCC 635

TGCCGTCCAG TCACGTGTGA CCTTGGGCAT GTCACCTCCC CTATCCTGGC TTCTGTATCT 695

TCTACAAAC AGGCTTCATT CCCCCAGGCC TGCTGGCTGG ACGGCTTTTA GGCCTGTCTG 755

AGGACCACGC CAGGAGCGCA AGGCAAAAC ACACCAGAGA T 796

<210> 37

<211> 29

<212> PRT

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 37

Ile Cys Cys Arg Cys Val Ser Pro Asp Gly Ile Pro Ser Asp Ile Thr  
1 5 10 15

Gly Ala Tyr Leu Glu Gly Trp Thr Val Leu His Arg Glu  
20 25

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<210> 38
<211> 634
<212> DNA
<213> Artificial Sequence
<200>
<223> Description of Artificial Sequence: Synthetic
        Primer

<220>
<221> CDS
<222> (326)..(499)

<400> 38
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CTAGAGAAAG CTGGGGCTGG TGGCCTCCAC CACAGGGAGA CGCAGACCCT CAGAAACAAG      120
TCTGTGAAGT CACAACCAGC CCCAGTTTAC AGATGTGAAA CTGAAGCTCC AAAAAGTCAG      180
GAGGTCACTG AGTGGGGAGG TGATGGAGTG GAACAGCCCC CAGATCTGGC TGAGGCCGAA      240
GCCCTGGAGA GATCCCCGCA AGGCTCCCTT AGATGCCTGA CATTCTGTTC TTCCTGAAGC      300
CTCACTCCCT TCTCTCCTGG CGCAG ACA CGT CCC CAT CAG AAG GCA CCA ACC      352
                Thr Arg Pro His Gln Lys Ala Pro Thr
                  1                      5

TCA ACG CGC CCA ACA GCC TGG GTG TCA GCG CCC TGT GTG CCA TCT GCG      400
Ser Thr Arg Pro Thr Ala Trp Val Ser Ala Pro Cys Val Pro Ser Ala
  10                      15                      20                      25

GGG ACC GGG CCA CGG GCA AAC ACT ACG GTG CCT CGA GCT GTG ACG GCT      448
Gly Thr Gly Pro Arg Ala Asn Thr Thr Val Pro Arg Ala Val Thr Ala
                30                      35                      40

GCA AGG GCT TCT TCC GGA GGA GCG TGC GGA AGA ACC ACA TGT ACT CCT      496
Ala Arg Ala Ser Ser Gly Gly Ala Cys Gly Arg Thr Thr Cys Thr Pro
          45                      50                      55

GCA GGTGAGGAGC CTCAATTTCT TCAGCTGGGA AATGGGCACA CTTGGGCTCA      549
Ala

TGGCCCCAAG GTCTGTCTTC TCCCTGAGTG GGTAGGTCCC AGAGACAGCT GCCCTTCAGG      609
GCCTTCAAGG CTCTTCTGGT TTTGT      634

<210> 39
<211> 58
<212> PRT
<213> Artificial Sequence
<200>
<223> Description of Artificial Sequence: Synthetic
        Peptide

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<211> 30  
 <212> PRT  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic Peptide  
  
 <400> 41  
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 1 5 10 15  
 Leu Gln Ala Gln Glu Met Leu Pro Gly Trp His Glu Glu Gly  
 20 25 30

<210> 42  
 <211> 662  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Description of Artificial Sequence: Synthetic Primer

<220>  
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 <222> (84)..(188)

<400> 42  
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 CACCTCTCTG TGCCTCCTCA CAG CCG TCC AGA ATG AGC GGG ACC GGA TCA 110  
 Pro Ser Arg Met Ser Gly Thr Gly Ser  
 1 5  
  
 GCA CTC GAA GGT CAA GCT ATG AGG ACA GCA GCC TGC CCT CCA TCA ATG 158  
 Ala Leu Glu Gly Gln Ala Met Arg Thr Ala Ala Cys Pro Pro Ser Met  
 10 15 20 25  
  
 CGC TCC TGC AGG CGG AGG TCC TGT CCC GAC AGGTACCGGG GTGATCCTGC 208  
 Arg Ser Cys Arg Arg Arg Ser Cys Pro Asp  
 30 35  
  
 CACCCACCCA GGGGATCCCC CACACTACAG AGGAGCTCAC CTCCTCCACC TCCATTCTCC 268  
  
 CCAGCCAGGC CCTGGAGCAG CTGACGGGAG GGGCCTCAGA TATTACAGAA GGGACACTGA 328  
  
 GTGCGGTTTC ACATGGCCCA GTTTGCAGCA AGGGCAGGAA TCGAACCTGG CGCCCTGGGG 388  
  
 CACTTTCTAA TTCATCCTAC TGCCTGCATC CCACAGGCCA AGCAGAGTCT TCACCTTCAC 448  
  
 TGAGGGCCTG CGATCAGCTC AGCTCCGAGA GAACAGAGCA GTGGCTCAGT GGAGAGAGGT 508  
  
 GGCAAAGTGG GGCCCAGCCC TTCCCTTGCT GAGTGACCTT GGGCAAGTCA CAGCACCTCT 568  
  
 CTGAGCCATG GTTGCTCAT TGTCAGAAAA GGATGATGAT TTTTGGCCCT GCTTCTCCTC 628  
  
 TAAGGCTGAC AGACTCCTTG GGGCTCTAAA GCTG 662

<210> 43  
 <211> 35  
 <212> PRT  
 <213> Artificial Sequence  
 <200>  
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 <400> 43  
 Pro Ser Arg Met Ser Gly Thr Gly Ser Ala Leu Glu Gly Gln Ala Met  
 1 5 10 15  
 Arg Thr Ala Ala Cys Pro Pro Ser Met Arg Ser Cys Arg Arg Arg Ser  
 20 25 30  
 Cys Pro Asp  
 35

<210> 44  
 <211> 647  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic Primer

<220>  
 <221> CDS  
 <222> (185)..(340)

<400> 44  
 TTCTCCCTCA TCCCTGCCTC CTCCCTCCCT CCGTTTTTAC CCTGAGCTTC CTTCAGAGCT 60  
 GGAGGGCACC CACTATCCAG CCCCTCCCC ACATCTGATT CCAGGGAGGG GGCTCTGTGC 120  
 AGGGGACAGA GAATGCGGGA GGGCCCGGAC ATCTCCAGCA TTTTCTTCCC TGTATCTCTC 180  
 GAAG ATC ACC TCC CCC GTC TCC GGG ATC AAC GGC GAC ATT CGG GCG AAG 229  
 Ile Thr Ser Pro Val Ser Gly Ile Asn Gly Asp Ile Arg Ala Lys 15  
 1 5 10 15  
 AAG ATT GCC AGC ATC GCA GAT GTG TGT GAG TCC ATG AAG GAG CAG CTG 277  
 Lys Ile Ala Ser Ile Ala Asp Val Cys Glu Ser Met Lys Glu Gln Leu 30  
 20 25 30  
 CTG GTT CTC GTT GAG TGG GCC AAG TAC ATC CCA GCT TTC TGC GAG CTC 325  
 Leu Val Leu Val Glu Trp Ala Lys Tyr Ile Pro Ala Phe Cys Glu Leu 45  
 35 40 45  
 CCC CTG GAC GAC CAG GTGAGGATGG GCGTGGATGG TGGGCAGTAG TGGGCAGTGG 380  
 Pro Leu Asp Asp Gln 50  
 50  
 GCGGGGCAGC CAGGGGGCTG CTGGCCCACC TGGGATATAG CCGTGGACTG GCTTGATTTT 440

ATTTTATTTA ACAAATATG TAGTGCACAC ACGTGTCTGA AACTTTAAAT CACCTTACAA 500  
 ATATTAAGCTC AGTTAGCTCC TCCAACAACCT CTATGAGGTA GGTACTAAGG TACTATTATT 560  
 ACTGCCATCT CATAGGTGAG AGATTGGGGC ACAGAGAGGT TAAGTAACCT GCTCAAGGTC 620  
 ACATAGCTAC TATCCAGCAT AGCTGGG 647

<210> 45  
 <211> 52  
 <212> PRT  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic Peptide

<400> 45  
 Ile Thr Ser Pro Val Ser Gly Ile Asn Gly Asp Ile Arg Ala Lys Lys  
 1 5 10 15  
 Ile Ala Ser Ile Ala Asp Val Cys Glu Ser Met Lys Glu Gln Leu Leu  
 20 25 30  
 Val Leu Val Glu Trp Ala Lys Tyr Ile Pro Ala Phe Cys Glu Leu Pro  
 35 40 45  
 Leu Asp Asp Gln  
 50

<210> 46  
 <211> 844  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic Primer  
 <220>  
 <221> CDS  
 <222> (429)..(515)

<400> 46  
 ATTTTACAA AGCACCTTC ATAATTCTCC ATAGCTGGTC CATGGGTGGG AATTGTTGGAC 60  
 CCACAGTTTT GGAAGTTTTT GGGATCATAG ACCTTTTTGA GAATCTCAA AAAGAAAAAA 120  
 AAGCACACAG AATGTTGCTT ACAGTTTCAT CAGGCACACA GAAGAGGCCC AGCACGAAGC 180  
 AGTTTCTTGC CCAAGGACAC AGCAGTTCAA GGACAGAGTC AGCGCGAGGT CTCTCAGCTC 240  
 TGAGCACATG TTCTTTCCCC TTCCAGGTTT CTAGTTTTAT GGGTAGTAGT TTTATGATGC 300  
 CCATTTTACA GTTCAGGCAG GTAGAGGCAG AGGGGAGCAT TAAGCTGACT TGCCCAGCGT 360  
 CACTGAGTTG GCTACGGGCA GCCTTCCCAA GGGTACAGAT GGCAAACACT GTTCCTTATC 420

TCTTTCAG GTG GCC CTG CTC AGA GCC CAT GCT GGC GAG CAC CTG CTG CTC 470  
Val Ala Leu Leu Arg Ala His Ala Gly Glu His Leu Leu Leu  
1 5 10

GGA GCC ACC AAG AGA TCC ATG GTG TTC AAG GAC GTG CTG CTC CTA 515  
Gly Ala Thr Lys Arg Ser Met Val Phe Lys Asp Val Leu Leu Leu  
15 20 25

GGTGAGGCGG CTGCCTGCCC TGGCCAGGGC TCCAGGGAGG GTATGCCTAG CATGGCACTC 575  
ACCCAGGCAA GGAGATTCAC ATGGTGGCAT GCAAGGGTGA GGGAGACTAG TCAGGAGTGG 635  
CCCTGTCCTC AGGCTTGTCAT TGGAGGGCTC CAGGACTCAG TTTTCAACTG GGTACCCAC 695  
TCAGATGCAA GGAAATGTGG ATGCAAGTCA CCAAATTCCTC AGCATTGAAG TCAGAGCACG 755  
ATCAGGGTTA TCCCTGGAAT TACCTGTGCA TCCTTTTTTC TTTTGACAGA GTCTTGCTCT 815  
GTCACCTCAGG CTGGAGTGCA ATGATGTGA 844

<210> 47  
<211> 29  
<212> PRT  
<213> Artificial Sequence  
<200>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 47  
Val Ala Leu Leu Arg Ala His Ala Gly Glu His Leu Leu Leu Gly Ala  
1 5 10 15  
Thr Lys Arg Ser Met Val Phe Lys Asp Val Leu Leu Leu  
20 25

<210> 48  
<211> 937  
<212> DNA  
<213> Artificial Sequence  
<200>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<221> CDS  
<222> (485) .. (529)

<220>  
<221> CDS  
<222> (533) .. (640)

<400> 48  
GCAACACTAG TATTTTAATA TAACAATGCT ATGAGGGAGC TCGATTATTT ATCCTCATCT 60  
TATAGATAAG AAAACTGAGG CACAGAGAGG TTAAGTAACT TATCCAATA TAACCAGCTA 120

TCAGGGGCAG AGCCATTTAA GCAGGGCAGT GCAGTTCAG AATCTGGTCC TTTAACCTTG 180

ATGCTTTGGT GCCTATCAGG TGACCTTTGA ATGTCATCGA TCTTGTGAGT CATGTTGGTA 240

AATGGAGCTT GGGTCATGTG AAAGAGGTCC TAGAAAGCCA AGTTCCAAGC TCAGCCGGAT 300

GACTCAAGGC AGCTTATCTT CTGAATCTGG GCCTCAGCTT CCTTACCTGT GAAATGGGAG 360

TCACCATCCC TGCAGGTCCT CCTCCACAG GCACCAGCTA TCTTGCCAAC TTAAAAGCCA 420

AAACTAGAGG AGAGGGGTCA ACCCAAAGTG ACTTCCCATC CTCCCTCCCT CCCAACCCCT 480

CCAG GCA ATG ACT ACA TTG TCC CTC GGC ACT GCC CGG AGC TGG CGG AGA 529  
Ala Met Thr Thr Leu Ser Leu Gly Thr Ala Arg Ser Trp Arg Arg  
1 5 10 15

TGA GCC GGG TGT CCA TAC GCA TCC TTG ACG AGC TGG TGC TGC CCT TCC 577  
Ala Gly Cys Pro Tyr Ala Ser Leu Thr Ser Trp Cys Cys Pro Ser  
20 25 30

AGG AGC TGC AGA TCG ATG ACA ATG AGT ATG CCT ACC TCA AAG CCA TCA 625  
Arg Ser Cys Arg Ser Met Thr Met Ser Met Pro Thr Ser Lys Pro Ser  
35 40 45

TCT TCT TTG ACC CAG GTACAGTGCA CACCTCCTAA GCCATCCCTG ACTCTCTCTC 680  
Ser Ser Leu Thr Gln  
50

CAGAACGCTC TGCCAGACTT CTCCTATTGG GTTCTGTACA CTGAGTTCAC AGCCTCATCT 740

CATGTTAACG ACAGCCAGGA GAGGCCGTTT TCATTTAACA GATGAGGCAA GTCAAGATTT 800

GAAGAGACAA TATGGCCGGG CGCAGTGGCT CACACCTGTA ATCCCATCAC TTTGGGAGGC 860

TGAGGCGGGC GGATCACCTG AGGTCAGGGG TCAAGATGAG CCTGGCTAAC ATGGAGAAAC 920

CCCATCTCTA CTTAAAA 937

<210> 49  
<211> 51  
<212> PRT  
<213> Artificial Sequence  
<200>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 49  
Ala Met Thr Thr Leu Ser Leu Gly Thr Ala Arg Ser Trp Arg Arg Ala  
1 5 10 15

Gly Cys Pro Tyr Ala Ser Leu Thr Ser Trp Cys Cys Pro Ser Arg Ser  
20 25 30

Cys Arg Ser Met Thr Met Ser Met Pro Thr Ser Lys Pro Ser Ser Ser  
35 40 45

Leu Thr Gln  
50

<210> 50  
<211> 978  
<212> DNA  
<213> Artificial Sequence  
<200>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<221> CDS  
<222> (376) .. (387)

<220>  
<221> CDS  
<222> (391) .. (432)

<220>  
<221> CDS  
<222> (436) .. (534)

<220>  
<221> CDS  
<222> (538) .. (610)

<400> 50  
GTGGCTCTGC CAACAACCTGG CTGTGCGACC CAGGACAAGT CCTATCTTTG CACTGTGTCT 60  
  
GGGTTTCCCC GTGTGTAAGA TGAGGCGGTT GCTAGGTGCT TATTGGATGC ATTCCTCAAG 120  
  
TCCCGCCCTC CATCTCCTAT TCCCCTCTCT TCTGGTTTAG TGCTTTAGGA AATGTGGCAG 180  
  
AAATCTTTTT CTGCCTGTGT CTAGGAAATC ATAATTCATG CTGGCGTACC CTGGTTGTTG 240  
  
AGGTCCCTGA ATCCTTGTGC CCACACTGCT GAAGACTCCT TGTGTGACAC AAGTCAGGGG 300  
  
ACATCTGGGT CTTGACTCCC CAGATGCTCC AGGTGGACCC TGCTGCCCTC CCTTGCCCAC 360  
  
CCTCTTCCAT TG TAG ATG CCA AGG GGC TGA GCG ATC CAG GGA AGA TCA AGC 411  
Met Pro Arg Gly Ala Ile Gln Gly Arg Ser Ser  
1 5 10  
  
GGC TGC GTT CCC AGG TGC AGG TGA GCT TGG AGG ACT ACA TCA ACG ACC 459  
Gly Cys Val Pro Arg Cys Arg Ala Trp Arg Thr Thr Ser Thr Thr  
15 20 25  
  
GCC AGT ATG ACT CGC GTG GCC GCT TTG GAG AGC TGC TGC TGC TGC TGC 507  
Ala Ser Met Thr Arg Val Ala Ala Leu Glu Ser Cys Cys Cys Cys Cys  
30 35 40  
  
CCA CCT TGC AGA GCA TCA CGT GGC AGA TGA TCG AGC AGA TCC AGT TCA 555  
Pro Pro Cys Arg Ala Ser Arg Gly Arg Ser Ser Arg Ser Ser Ser  
45 50 55

TCA AGC TCT TCG GCA TGG CCA AGA TTG ACA ACC TGT TGG AGG AGA TGC 603  
 Ser Ser Ser Ser Ala Trp Pro Arg Leu Thr Thr Cys Trp Arg Arg Cys  
           60                          65                          70

TGC TGG GAGGTCCGTG CCAAGCCCAG GAGGGGCGGG GTTGGATTGG GGACTCCCCA 659  
 Cys Trp  
       75

GGAGACAGGC CTCACACAGT GAGCTCACCC CTCAGCTCCT TGGCTTCCCC ACTGTGCCGC 719

TTTGGGCAAG TTGCTTAACC TGTCTGTGCC TCAGTTTCCT CACCAGAAAA ATGGGAACAA 779

GGCAATGGTC TATTTGTTCA GGCACCGAGA ACCTAGCACG TGCCAGTCAC TGTTCTAAGT 839

GCTGGCAATT CAGCAAAGAA CAAGATCTTT GCCCTCGGGG AGGCTGTGTG TGTGTGATAT 899

GTATGGATGC GTGGATATCT GTGTATATGC CCGTATGTGC GTGCATGTGT ATATAAAGCC 959

TCACATTTTA TGATTTTGA 978

<210> 51

<211> 75

<212> PRT

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
 Peptide

<400> 51

Met Pro Arg Gly Ala Ile Gln Gly Arg Ser Ser Gly Cys Val Pro Arg  
   1                          5                          10                          15

Cys Arg Ala Trp Arg Thr Thr Ser Thr Thr Ala Ser Met Thr Arg Val  
                           20                          25                          30

Ala Ala Leu Glu Ser Cys Cys Cys Cys Cys Pro Pro Cys Arg Ala Ser  
                           35                          40                          45

Arg Gly Arg Ser Ser Arg Ser Ser Ser Ser Ser Ser Ser Ala Trp Pro  
                           50                          55                          60

Arg Leu Thr Thr Cys Trp Arg Arg Cys Cys Trp  
   65                          70                          75

<210> 52

<211> 984

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
 Primer

<220>

<221> CDS

<222> (443) .. (490)

<220>  
 <221> CDS  
 <222> (494) .. (595)  
  
 <400> 52  
 GGGACACATA GATGCTATAA GTAGGTCAGT TGGCTGCAGC AGAGATGTGG GGGATGAGGC 60  
 TGAAAGGTGA GGC GGGACCA AATGGTTGAA GGACTTGCAC TCCAAGGAGC TTTGAGAGCC 120  
 ATTGATTACA TCCATTATGT TACTATGTGA CCAATACATT ACTCATTAGA ACATTTACGT 180  
 GATCTCAGAG CTTCTTATA TGCACCTTGT TCCTTTCAAC TCACTTTTGT TCTCTTGGTT 240  
 TTTTGGGGTC CTCTTAACAC CCTCATGAAG TCTATAGATG GGAATGGTAC ACCCTAGTTT 300  
 ACTAACCCAG GAATAGGTAC CCAACAGGCA CTGCCAATAT TGGATGGGCT GGTTGATTGG 360  
 CCACGCCTGA GGAAGATGGC GTCCCAAGGC CTGAGGTCTG CATCCCAGAC TCTCCATCCT 420  
 GATCGACCTT CTCTACCTGC AG GGT CCC CCA GCG ATG CAC CCC ATG CCC ACC 472  
    Gly Pro Pro Ala Met His Pro Met Pro Thr  
    1   5   10  
 ACC CCC TGC ACC CTC ACC TGA TGC AGG AAC ATA TGG GAA CCA ACG TCA 520  
 Thr Pro Cys Thr Leu Thr Cys Arg Asn Ile Trp Glu Pro Thr Ser  
    15   20   25  
 TCG TTG CCA ACA CAA TGC CCA CTC ACC TCA GCA ACG GAC AGA TGT GTG 568  
 Ser Leu Pro Thr Gln Cys Pro Leu Thr Ser Ala Thr Asp Arg Cys Val  
    30   35   40  
 AGT GGC CCC GAC CCA GGG GAC AGG CAG GTGGGCAAAC TCTGGGATTT 615  
 Ser Gly Pro Asp Pro Gly Asp Arg Gln  
    45   50  
 TACCTTGCAA AGGGTGAGGA TGGGGCTTAA GACAGGAGGC AGGAGAAAGT GGAGTCTAGA 675  
 AGGTAGAACC AGGATGCAAC AGTTTTCTGG GTTCCAGGGT AGGGAATAAA GGGCAAGATT 735  
 GTCCATTTGT TGAGGCTGTT TATTCAGTAA GGTGACTGAC AGCCTTTACT GAATGAAGCC 795  
 ATTGTTGGGA TGAGGCAATC CACTGGATGA GGTAACCCAT TGGGTGAAGA TGTCTTGGGT 855  
 GAGAATTCCA TTAGTTGACA TTGTCCATTA AGTAAAAGTG GTCATTGAAG TAAGGCTGCA 915  
 CAGTTGGGTA AGGCTATCCA TTAGACATTA GATGAGACTA CCCATTGGGT CAGGATGTCT 975  
 GCTGGGCTA 984  
  
 <210> 53  
 <211> 50  
 <212> PRT  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic Peptide



<400> 53

Gly Pro Pro Ala Met His Pro Met Pro Thr Thr Pro Cys Thr Leu Thr  
1 5 10 15

Cys Arg Asn Ile Trp Glu Pro Thr Ser Ser Leu Pro Thr Gln Cys Pro  
20 25 30

Leu Thr Ser Ala Thr Asp Arg Cys Val Ser Gly Pro Asp Pro Gly Asp  
35 40 45

Arg Gln  
50

<210> 54

<211> 1103

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> CDS

<222> (289) .. (429)

<220>

<221> CDS

<222> (433) .. (477)

<220>

<221> CDS

<222> (481) .. (492)

<220>

<221> CDS

<222> (496) .. (603)

<220>

<221> CDS

<222> (607) .. (630)

<220>

<221> CDS

<222> (634) .. (750)

<220>

<221> CDS

<222> (754) .. (810)

<220>

<221> CDS

<222> (814) .. (843)

<220>

<221> CDS  
 <222> (847)..(1023)

<220>  
 <221> CDS  
 <222> (1027)..(1071)

<220>  
 <221> CDS  
 <222> (1075)..(1103)

<400> 54  
 TTTGGGAGAA GCAGTCCAAG TCTGCATATC AAATAAATGA TGGAGGAGAT GGGTGGTAGG 60  
 ACCTTCCAGA CCTCATAAAA CTTAGGCTTT ATGATCTGGG ACTCACAGAA GGTTGAGCAA 120  
 TAAAAGACCT TAGGGATTAT CTGGCTTAAT TAATTCTCTC ATTTTATAGA GGAAGAAATT 180  
 AAGTCAAGGT GGGGCAGGGT GGGAGGGGAG AACTTTCCCG GGGCTCTTCA TTTACTCCCA 240  
 CAAAGGCTGG AATTTTGAGC AGCCCCTGTC TGTCTGTTTG TCCTTCCA GCC ACC CCT 297  
 Ala Thr Pro  
 1  
 GAG ACC CCA CAG CCC TCA CCG CCA GGT GGC TCA GGG TCT GAG CCC TAT 345  
 Glu Thr Pro Gln Pro Ser Pro Pro Gly Gly Ser Gly Ser Glu Pro Tyr  
 5 10 15  
 AAG CTC CTG CCG GGA GCC GTC GCC ACA ATC GTC AAG CCC CTC TCT GCC 393  
 Lys Leu Leu Pro Gly Ala Val Ala Thr Ile Val Lys Pro Leu Ser Ala  
 20 25 30 35  
 ATC CCC CAG CCG ACC ATC ACC AAG CAG GAA GTT ATC TAG CAA GCC GCT 441  
 Ile Pro Gln Pro Thr Ile Thr Lys Gln Glu Val Ile Gln Ala Ala  
 40 45 50  
 GGG GCT TGG GGG CTC CAC TGG CTC CCC CCA GCC CCC TAA GAG AGC ACC 489  
 Gly Ala Trp Gly Leu His Trp Leu Pro Pro Ala Pro Glu Ser Thr  
 55 60 65  
 TGG TGA TCA CGT GGT CAC GGC AAA GGA AGA CGT GAT GCC AGG ACC AGT 537  
 Trp Ser Arg Gly His Gly Lys Gly Arg Arg Asp Ala Arg Thr Ser  
 70 75 80  
 CCC AGA GCA GGA ATG GGA AGG ATG AAG GGC CCG AGA ACA TGG CCT AAG 585  
 Pro Arg Ala Gly Met Gly Arg Met Lys Gly Pro Arg Thr Trp Pro Lys  
 85 90 95  
 GCA CAT CCC ACT GCA CCC TGA CGC CCT GCT CTG ATA ACA AGA CTT 630  
 Ala His Pro Thr Ala Pro Arg Pro Ala Leu Ile Thr Arg Leu  
 100 105 110  
 TGA CTT GGG GAG ACC CTC TAC TGC CTT GGA CAA CTT TCT CAT GTT GAA 678  
 Leu Gly Glu Thr Leu Tyr Cys Leu Gly Gln Leu Ser His Val Glu  
 115 120 125

GCC ACT GCC TTC ACC TTC ACC TTC ATC CAT GTC CAA CCC CCG ACT TCA	726
Ala Thr Ala Phe Thr Phe Thr Phe Ile His Val Gln Pro Pro Thr Ser	
130 135 140	
TCC CAA AGG ACA GCC GCC TGG AGA TGA CTT GAG CCT TAC TTA AAC CCA	774
Ser Gln Arg Thr Ala Ala Trp Arg Leu Glu Pro Tyr Leu Asn Pro	
145 150 155	
GCT CCC TTC TTC CCT AGC CTG GTG CTT CTC CTC TCC TAG CCC CGG TCA	822
Ala Pro Phe Phe Pro Ser Leu Val Leu Leu Ser Pro Arg Ser	
160 165 170	
TGG TGT CCA GAC AGA GCC CTG TGA GGC TGG GTC CAA TTG TGG CAC TTG	870
Trp Cys Pro Asp Arg Ala Leu Gly Trp Val Gln Leu Trp His Leu	
175 180 185	
GGG CAC CTT GCT CCT CCT TCT GCT GCT GCC CCC ACC TCT GCT GCC TCC	918
Gly His Leu Ala Pro Pro Ser Ala Ala Ala Pro Thr Ser Ala Ala Ser	
190 195 200	
CTC TGC TGT CAC CTT GCT CAG CCA TCC CGT CTT CTC CAA CAC CAC CTC	966
Leu Cys Cys His Leu Ala Gln Pro Ser Arg Leu Leu Gln His His Leu	
205 210 215	
TAC AGA GGC CAA GGA GGC CTT GGA AAC GAT TCC CCC AGT CAT TCT GGG	1014
Tyr Arg Gly Gln Gly Gly Leu Gly Asn Asp Ser Pro Ser His Ser Gly	
220 225 230	
AAC ATG TTG TAA GCA CTG ACT GGG ACC AGG CAC CAG GCA GGG TCT AGA	1062
Asn Met Leu Ala Leu Thr Gly Thr Arg His Gln Ala Gly Ser Arg	
235 240 245	
AGG CTG TGG TGA GGG AAG ACG CCT TTC TCC TCC AAC CCA AC	1103
Arg Leu Trp Gly Lys Thr Pro Phe Ser Ser Asn Pro	
250 255 260	
<210> 55	
<211> 261	
<212> PRT	
<213> Artificial Sequence	
<200>	
<223> Description of Artificial Sequence: Synthetic Peptide	
<400> 55	
Ala Thr Pro Glu Thr Pro Gln Pro Ser Pro Pro Gly Gly Ser Gly Ser	
1 5 10 15	
Glu Pro Tyr Lys Leu Leu Pro Gly Ala Val Ala Thr Ile Val Lys Pro	
20 25 30	
Leu Ser Ala Ile Pro Gln Pro Thr Ile Thr Lys Gln Glu Val Ile Gln	
35 40 45	
Ala Ala Gly Ala Trp Gly Leu His Trp Leu Pro Pro Ala Pro Glu Ser	
50 55 60	

Thr Trp Ser Arg Gly His Gly Lys Gly Arg Arg Asp Ala Arg Thr Ser  
 65 70 75 80  
 Pro Arg Ala Gly Met Gly Arg Met Lys Gly Pro Arg Thr Trp Pro Lys  
 85 90 95  
 Ala His Pro Thr Ala Pro Arg Pro Ala Leu Ile Thr Arg Leu Leu Gly  
 100 105 110  
 Glu Thr Leu Tyr Cys Leu Gly Gln Leu Ser His Val Glu Ala Thr Ala  
 115 120 125  
 Phe Thr Phe Thr Phe Ile His Val Gln Pro Pro Thr Ser Ser Gln Arg  
 130 135 140  
 Thr Ala Ala Trp Arg Leu Glu Pro Tyr Leu Asn Pro Ala Pro Phe Phe  
 145 150 155 160  
 Pro Ser Leu Val Leu Leu Leu Ser Pro Arg Ser Trp Cys Pro Asp Arg  
 165 170 175  
 Ala Leu Gly Trp Val Gln Leu Trp His Leu Gly His Leu Ala Pro Pro  
 180 185 190  
 Ser Ala Ala Ala Pro Thr Ser Ala Ala Ser Leu Cys Cys His Leu Ala  
 195 200 205  
 Gln Pro Ser Arg Leu Leu Gln His His Leu Tyr Arg Gly Gln Gly Gly  
 210 215 220  
 Leu Gly Asn Asp Ser Pro Ser His Ser Gly Asn Met Leu Ala Leu Thr  
 225 230 235 240  
 Gly Thr Arg His Gln Ala Gly Ser Arg Arg Leu Trp Gly Lys Thr Pro  
 245 250 255  
 Phe Ser Ser Asn Pro  
 260

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 56

GGGCACTGGG AGGAGGCAGT

20

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 57  
 GCCTGTAGGA CCAACCTACC 20

<210> 58  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 58  
 TCTGGTGTGC ACGACTGCAC 20

<210> 59  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 59  
 CTGGAGCTGC AGCCTCATAC 20

<210> 60  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 60  
 AAGGCTCCCT TAGATGCCTG 20

<210> 61  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 61  
 CCACTCAGGG AGAAGACAGA CCT 23

<210> 62  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <200>

<223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 62  
 CCTAGTTCTG TCCTAAGAGG 20

<210> 63  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 63  
 GTCATAAAGT GTGGCTACAG 20

<210> 64  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 64  
 CCACCCCCTA CTCCATCCCT GT 22

<210> 65  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 65  
 CCCTCCCGTC AGCTGCTCCA 20

<210> 66  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 66  
 GTGCAGGGGA CAGAGAATGC 20

<210> 67  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
 <200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 67

AATCAAGCCA GTCCACGGCT AT

22

<210> 68

<211> 23

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 68

GCCCAGCGTC ACTGAGTTGG CTA

23

<210> 69

<211> 20

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 69

TTGCCTGGGT GAGTGCCATG

20

<210> 70

<211> 20

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 70

GCACCAGCTA TCTTGCCAAC

20

<210> 71

<211> 20

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 71

AGGAGAAGTC TGGCAGAGCG

20

<210> 72

<211> 20

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 72  
CTCCTTGTGT GACACAAGTC 20

<210> 73  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 73  
CTCACTGTGT GAGGCCTGTC 20

<210> 74  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 74  
TGGTTGATTG GCCACGCCTG 20

<210> 75  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 75  
ATCCTGGTTC TACCTTCTAG 20

<210> 76  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 76  
CATTTACTCC CACAAAGGCT 20

<210> 77  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<200>



<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 77  
GACCACGTGA TCACCAGGTG 20

<210> 78  
<211> 1441  
<212> DNA  
<213> Artificial Sequence  
<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<221> CDS  
<222> (20)..(1414)

<400> 78  
CTCCAAAACC CTCGTCGAC ATG GAC ATG GCC GAC TAC AGT GCT GCA CTG GAC 52  
Met Asp Met Ala Asp Tyr Ser Ala Ala Leu Asp  
1 5 10

CCA GCC TAC ACC ACC CTG GAA TTT GAG AAT GTG CAG GTG TTG ACG ATG 100  
Pro Ala Tyr Thr Thr Leu Glu Phe Glu Asn Val Gln Val Leu Thr Met  
15 20 25

GGC AAT GAC ACG TCC CCA TCA GAA GGC ACC AAC CTC AAC GCG CCC AAC 148  
Gly Asn Asp Thr Ser Pro Ser Glu Gly Thr Asn Leu Asn Ala Pro Asn  
30 35 40

AGC CTG GGT GTC AGC GCC CTG TGT GCC ATC TGC GGG GAC CGG GCC ACG 196  
Ser Leu Gly Val Ser Ala Leu Cys Ala Ile Cys Gly Asp Arg Ala Thr  
45 50 55

GGC AAA CAC TAC GGT GCC TCG AGC TGT GAC GGC TGC AAG GGC TTC TTC 244  
Gly Lys His Tyr Gly Ala Ser Ser Cys Asp Gly Cys Lys Gly Phe Phe  
60 65 70 75

CGG AGG AGC GTG CGG AAG AAC CAC ATG TAC TCC TGC AGA TTT AGC CGG 292  
Arg Arg Ser Val Arg Lys Asn His Met Tyr Ser Cys Arg Phe Ser Arg  
80 85 90

CAG TGC GTG GTG GAC AAA GAC AAG AGG AAC CAG TGC CGC TAC TGC AGG 340  
Gln Cys Val Val Asp Lys Asp Lys Arg Asn Gln Cys Arg Tyr Cys Arg  
95 100 105

CTC AAG AAA TGC TTC CGG GCT GGC ATG AAG AAG GAA GCC GTC CAG AAT 388  
Leu Lys Lys Cys Phe Arg Ala Gly Met Lys Lys Glu Ala Val Gln Asn  
110 115 120

GAG CGG GAC CGG ATC AGC ACT CGA AGG TCA AGC TAT GAG GAC AGC AGC 436  
Glu Arg Asp Arg Ile Ser Thr Arg Arg Ser Ser Tyr Glu Asp Ser Ser  
125 130 135

CTG CCC TCC ATC AAT GCG CTC CTG CAG GCG GAG GTC CTG TCC CGA CAG 484

Leu 140	Pro	Ser	Ile	Asn	Ala 145	Leu	Leu	Gln	Ala	Glu 150	Val	Leu	Ser	Arg	Gln 155	
ATC Ile	ACC Thr	TCC Ser	CCC Pro	GTC Val	TCC Ser	GGG Gly	ATC Ile	AAC Asn	GGC Gly	GAC Asp	ATT Ile	CGG Arg	GCG Ala	AAG Lys	AAG Lys	532
ATT Ile	GCC Ala	AGC Ser	ATC Ile	GCA Ala	GAT Asp	GTG Val	TGT Cys	GAG Glu	TCC Ser	ATG Met	AAG Lys	GAG Glu	CAG Gln	CTG Leu	CTG Leu	580
GTT Val	CTC Leu	GTT Val	GAG Glu	TGG Trp	GCC Ala	AAG Lys	TAC Tyr	ATC Ile	CCA Pro	GCT Ala	TTC Phe	TGC Cys	GAG Glu	CTC Leu	CCC Pro	628
CTG Leu	GAC Asp	GAC Asp	CAG Gln	GTG Val	GCC Ala	CTG Leu	CTC Leu	AGA Arg	GCC Ala	CAT His	GCT Ala	GGC Gly	GAG Glu	CAC His	CTG Leu	676
CTG Leu	CTC Leu	GGA Gly	GCC Ala	ACC Thr	AAG Lys	AGA Arg	TCC Ser	ATG Met	GTG Val	TTC Phe	AAG Lys	GAC Asp	GTG Val	CTG Leu	CTC Leu	724
CTA Leu	GGC Gly	AAT Asn	GAC Asp	TAC Tyr	ATT Ile	GTC Val	CCT Pro	CGG Arg	CAC His	TGC Cys	CCG Pro	GAG Glu	CTG Leu	GCG Ala	GAG Glu	772
ATG Met	AGC Ser	CGG Arg	GTG Val	TCC Ser	ATA Ile	CGC Arg	ATC Ile	CTT Leu	GAC Asp	GAG Glu	CTG Leu	GTG Val	CTG Leu	CCC Pro	TTC Phe	820
CAG Gln	GAG Glu	CTG Leu	CAG Gln	ATC Ile	GAT Asp	GAC Asp	AAT Asn	GAG Glu	TAT Tyr	GCC Ala	TAC Tyr	CTC Leu	AAA Lys	GCC Ala	ATC Ile	868
ATC Ile	TTC Phe	TTT Phe	GAC Asp	CCA Pro	GAT Asp	GCC Ala	AAG Lys	GGG Gly	CTG Leu	AGC Ser	GAT Asp	CCA Pro	GGG Gly	AAG Lys	ATC Ile	916
AAG Lys	CGG Arg	CTG Leu	CGT Arg	TCC Ser	CAG Gln	GTG Val	CAG Gln	GTG Val	AGC Ser	TTG Leu	GAG Glu	GAC Asp	TAC Tyr	ATC Ile	AAC Asn	964
GAC Asp	CGC Arg	CAG Gln	TAT Tyr	GAC Asp	TCG Ser	CGT Arg	GGC Gly	CGC Arg	TTT Phe	GGA Gly	GAG Glu	CTG Leu	CTG Leu	CTG Leu	CTG Leu	1012
CTG Leu	CCC Pro	ACC Thr	TTG Leu	CAG Gln	AGC Ser	ATC Ile	ACC Thr	TGG Trp	CAG Gln	ATG Met	ATC Ile	GAG Glu	CAG Gln	ATC Ile	CAG Gln	1060
TTC Phe	ATC Ile	AAG Lys	CTC Leu	TTC Phe	GGC Gly	ATG Met	GCC Ala	AAG Lys	ATT Ile	GAC Asp	AAC Asn	CTG Leu	TTG Leu	CAG Gln	GAG Glu	1108
ATG Met	CTG Leu	CTG Leu	GGA Gly	GGG Gly	TCC Ser	CCC Pro	AGC Ser	GAT Asp	GCA Ala	CCC Pro	CAT His	GCC Ala	CAC His	CAC His	CCC Pro	1156

365	370	375	
CTG CAC CCT CAC CTG ATG CAG GAA CAT ATG GGA ACC AAC GTC ATC GTT			1204
Leu His Pro His Leu Met Gln Glu His Met Gly Thr Asn Val Ile Val			
380	385	390	395
GCC AAC ACA ATG CCC ACT CAC CTC AGC AAC GGA CAG ATG TGT GAG TGG			1252
Ala Asn Thr Met Pro Thr His Leu Ser Asn Gly Gln Met Cys Glu Trp			
	400	405	410
CCC CGA CCC AGG GGA CAG GCA GCC ACC CCT GAG ACC CCA CAG CCC TCA			1300
Pro Arg Pro Arg Gly Gln Ala Ala Thr Pro Glu Thr Pro Gln Pro Ser			
	415	420	425
CCG CCA GGT GCG TCA GGG TCT GAG CCC TAT AAG CTC CTG CCG GGA GCC			1348
Pro Pro Gly Ala Ser Gly Ser Glu Pro Tyr Lys Leu Leu Pro Gly Ala			
	430	435	440
GTC GCC ACA ATC GTC AAG CCC CTC TCT GCC ATC CCC CAG CCG ACC ATC			1396
Val Ala Thr Ile Val Lys Pro Leu Ser Ala Ile Pro Gln Pro Thr Ile			
	445	450	455
ACC AAG CAG GAA GTT ATC TAGCAAGCCG CTGGGGCTTG GGGGCTC			1441
Thr Lys Gln Glu Val Ile			
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Leu Glu Phe Glu Asn Val Gln Val Leu Thr Met Gly Asn Asp Thr Ser			
	20	25	30
Pro Ser Glu Gly Thr Asn Leu Asn Ala Pro Asn Ser Leu Gly Val Ser			
	35	40	45
Ala Leu Cys Ala Ile Cys Gly Asp Arg Ala Thr Gly Lys His Tyr Gly			
	50	55	60
Ala Ser Ser Cys Asp Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Arg			
	65	70	75
Lys Asn His Met Tyr Ser Cys Arg Phe Ser Arg Gln Cys Val Val Asp			
	85	90	95
Lys Asp Lys Arg Asn Gln Cys Arg Tyr Cys Arg Leu Lys Lys Cys Phe			
	100	105	110

Arg Ala Gly Met Lys Lys Glu Ala Val Gln Asn Glu Arg Asp Arg Ile  
 115 120 125  
 Ser Thr Arg Arg Ser Ser Tyr Glu Asp Ser Ser Leu Pro Ser Ile Asn  
 130 135 140  
 Ala Leu Leu Gln Ala Glu Val Leu Ser Arg Gln Ile Thr Ser Pro Val  
 145 150 155 160  
 Ser Gly Ile Asn Gly Asp Ile Arg Ala Lys Lys Ile Ala Ser Ile Ala  
 165 170 175  
 Asp Val Cys Glu Ser Met Lys Glu Gln Leu Leu Val Leu Val Glu Trp  
 180 185 190  
 Ala Lys Tyr Ile Pro Ala Phe Cys Glu Leu Pro Leu Asp Asp Gln Val  
 195 200 205  
 Ala Leu Leu Arg Ala His Ala Gly Glu His Leu Leu Leu Gly Ala Thr  
 210 215 220  
 Lys Arg Ser Met Val Phe Lys Asp Val Leu Leu Leu Gly Asn Asp Tyr  
 225 230 235 240  
 Ile Val Pro Arg His Cys Pro Glu Leu Ala Glu Met Ser Arg Val Ser  
 245 250 255  
 Ile Arg Ile Leu Asp Glu Leu Val Leu Pro Phe Gln Glu Leu Gln Ile  
 260 265 270  
 Asp Asp Asn Glu Tyr Ala Tyr Leu Lys Ala Ile Ile Phe Phe Asp Pro  
 275 280 285  
 Asp Ala Lys Gly Leu Ser Asp Pro Gly Lys Ile Lys Arg Leu Arg Ser  
 290 295 300  
 Gln Val Gln Val Ser Leu Glu Asp Tyr Ile Asn Asp Arg Gln Tyr Asp  
 305 310 315 320  
 Ser Arg Gly Arg Phe Gly Glu Leu Leu Leu Leu Leu Pro Thr Leu Gln  
 325 330 335  
 Ser Ile Thr Trp Gln Met Ile Glu Gln Ile Gln Phe Ile Lys Leu Phe  
 340 345 350  
 Gly Met Ala Lys Ile Asp Asn Leu Leu Gln Glu Met Leu Leu Gly Gly  
 355 360 365  
 Ser Pro Ser Asp Ala Pro His Ala His His Pro Leu His Pro His Leu  
 370 375 380  
 Met Gln Glu His Met Gly Thr Asn Val Ile Val Ala Asn Thr Met Pro  
 385 390 395 400  
 Thr His Leu Ser Asn Gly Gln Met Cys Glu Trp Pro Arg Pro Arg Gly  
 405 410 415

Gln Ala Ala Thr Pro Glu Thr Pro Gln Pro Ser Pro Pro Gly Ala Ser  
420 425 430

Gly Ser Glu Pro Tyr Lys Leu Leu Pro Gly Ala Val Ala Thr Ile Val  
435 440 445

Lys Pro Leu Ser Ala Ile Pro Gln Pro Thr Ile Thr Lys Gln Glu Val  
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Ile  
465

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<211> 2329  
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Primer

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GCTAGTGGGG TTTTGGGGGG GCAGTGGGTG CAAGGAGTTT GGTTTGTGTC TGCCGGCCGG 120  
CAGGCAAACG CAACCACGCG GTGGGGGAGG CGGCTAGCGT GGTGGACGGC CCGCGTGGCC 180  
CTGTGGCAGC CGAGCCATGG TTTCTAAACT GAGCCAGCTG CAGACGGAGC TCCTGGCGGC 240  
CCTGCTCGAG TCAGGGCTGA GCAAAGAGGC ACTGATCCAG GCACTGGGTG AGCCGGGGCC 300  
CTACCTCCTG GCTGGAGAAG GCCCCCTGGA CAAGGGGGAG TCCTGCGGCG GCGGTCGAGG 360  
GGAGCTGGCT GAGCTGCCCA ATGGGCTGGG GGAGACTCGG GGCTCCGAGG ACGAGACGGA 420  
CGACGATGGG GAAGACTTCA CGCCACCCAT CCTCAAAGAG CTGGAGAACC TCAGCCCTGA 480  
GGAGGCGGCC CACCAGAAAAG CCGTGGTGGA GACCTTCTG CAGGAGGACC CGTGGCGTGT 540  
GGCGAAGATG GTCAAGTCCT ACCTGCAGCA GCACAACATC CCACAGCGGG AGGTGGTCGA 600  
TACCACTGGC CTCAACCAGT CCCACCTGTC CCAACACCTC AACAAGGGCA CTCCCATGAA 660  
GACGCAGAAG CGGGCCGCCC TGTACACCTG GTACGTCCGC AAGCAGCGAG AGGTGGCGCA 720  
GCAGTTCACC CATGCAGGGC AGGGAGGGCT GATTGAAGAG CCCACAGGTG ATGAGCTACC 780  
AACCAAGAAG GGGCGGAGGA ACCGTTTCAA GTGGGGCCCA GCATCCCAGC AGATCCTGTT 840  
CCAGGCCTAT GAGAGGCAGA AGAACCTAG CAAGGAGGAG CGAGAGACGC TAGTGGAGGA 900  
GTGCAATAGG GCGGAATGCA TCCAGAGAGG GGTGTCCCA TCACAGGCAC AGGGGCTGGG 960  
CTCCAACCTC GTCACGGAGG TGCCTGTCTA CAACTGGTTT GCCAACCAGC GCAAAGAAGA 1020  
AGCCTTCCGG CACAAGCTGG CCATGGACAC GTACAGCGGG CCCCCCCAG GGCCAGGCCC 1080

GGGACCTGCG CTGCCCCTC ACAGCTCCCC TGGCCTGCCT CCACCTGCCC TCTCCCCCAG	1140
TAAGGTCCAC GGTGTGCGCT ATGGACAGCC TGCACCAGT GAGACTGCAG AAGTACCCTC	1200
AAGCAGCGGC GGTCCCTTAG TGACAGTGTC TACACCCTC CACCAAGTGT CCCCCACGGG	1260
CCTGGAGCCC AGCCACAGCC TGCTGAGTAC AGAAGCCAAG CTGGTCTCAG CAGCTGGGGG	1320
CCCCCTCCCC CCTGTCAGCA CCCTGACAGC ACTGCACAGC TTGGAGCAGA CATCCCCAGG	1380
CCTCAACCAG CAGCCCCAGA ACCTCATCAT GGCCTCACTT CCTGGGGTCA TGACCATCGG	1440
GCCTGGTGAG CCTGCCTCCC TGGGTCTTAC GTTCACCAAC ACAGGTGCCT CCACCCTGGT	1500
CATCGGCCTG GCCTCCACGC AGGCACAGAG TGTGCCGGTC ATCAACAGCA TGGGCAGCAG	1560
CCTGACCACC CTGCAGCCCG TCCAGTTCTC CCAGCCGCTG CACCCCTCCT ACCAGCAGCC	1620
GCTCATGCCA CCTGTGCAGA GCCATGTGAC CCAGAGCCCC TTCATGGCCA CCATGGCTCA	1680
GCTGCAGAGC CCCCACGGTG AGCACCTGT GCCCCACACA GCAGGAGATG ATGATAGAGG	1740
TTGGCTGTCA ATGGATGCAG GGGAAAGGGG TGCCTGGCAG GCATTGCAGT CTGCATGTGT	1800
CTCTGGGACA AGTGTTTTTC CGTGATTGAG GGTGTCTGCA GGCCAGTGTG TTCCCATGTG	1860
AATGCACGTA TCTGTGTGTG TGCACGACTG CTTGTGTGAG CAGATCCCTA GTCGTGTCTG	1920
GGTGTGTATC GGTGTGTCAT GCATTTGTGT GCATCCTGTG TTTCTCTGAA ACTCTTAGGG	1980
CCATATGAAT TTCTAAAATC TATTCAGATT TTAGAAAGGT AATCTGGGGC CAGGCGTGGT	2040
GGCTCATGCC TGTAATCCCA GCACTTTGGA AGGCCGAGGT GGGCAGATCA CTTGAGGTCA	2100
GGAGTTCAAG ACCAGCCTGG CCAACACGGT GAAACCCCGT CTCTACTAAA AGTACAAAAA	2160
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GCTTGAACCT GGGAGGCGGA GGTTCAGTG AGCTGAGATT TGGCCACTGC ACTGCACTCC	2280
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<211> 20

<212> DNA

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<223> Description of Artificial Sequence: Synthetic  
Primer

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<210> 82

<211> 20

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20

<210> 83  
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Peptide

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1 5

<210> 84  
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1 5

<210> 85  
<211> 5  
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Peptide

<400> 85  
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1 5

<210> 86  
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<400> 86

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36

<210> 87

<211> 12

<212> PRT

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<223> Description of Artificial Sequence: Synthetic  
Peptide

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Asp Thr Tyr Ser Gly Pro Pro Pro Gly Pro Gly Pro  
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<210> 88

<211> 36

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Asp Thr Tyr Ser Gly Pro Pro Pro Arg Ala Arg Pro  
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<210> 124 <211> 23 <212> DNA <213> Artificial Sequence <200> <223> Description of Artificial Sequence: Synthetic Primer	
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<210> 126  
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<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
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<222> (1287)..(4273)  
<223> N = A, C, G, or T

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GTGTCAGGCC GGGAGTGGGG TGGAAGGGTC CCAAAATGGA TGGAAGGGCC CCAAAATGGC 120  
CGTGAGCATC CTCTGCCCTT GAGAAGAGCT AGCCCAGCTG TCTAGAGCTC CCTGCTGCTG 180  
CCGCTCTCGT AAGCAGCAAG CATTTTGGC TCTCCTGTCT CAGCATGATG CCCCTACAAG 240  
GTTCTTTCGG GGGTGGGACC CAACGCTGCT CTCCTGATGG CCTCCCTGGC TCCCAGCACC 300  
TTCCATCCCA GCTGCTCAGG GCCCCTCACC TGCGCCTCCC CCACCCTCCC CTCTGCCCAC 360  
TCCCATCGCA GGCCATAGCT CCCTGTCCCT CTCCGCTGCC ATGAGGCCTG CACTTTGCAG 420  
GGCTGAAGTC CAAAGTTCAG TCCCTTCGCT AAGCACACGG ATAAATATGA ACCTTGAGAG 480  
ATTTCCCCAG CTCCAATGTA AACAGAACAG GCAGGGGGCCC TGATTACAGG GCCGCTGGGG 540  
CCAGGGTTGG GGGTTGGGGG TGCCCACAGG GCTTGGCTAG TGGGGTTTTG GGGGGGCAGT 600  
GGGTGCAAGG AGTTTGGTTT GTGTCTGCCG GCCGGCAGGC AAACGCAACC CACGCGGTGG 660  
GGGAGGCGGC TAGCGTGGTG GACCCGGGCC GCGTGGCCCT GTGGCAGCCG AGCCATGGTT 720  
TCTAAACTGA GCCAGCTGCA GACGGAGCTC CTGGCGGCCC TGCTCGAGTC AGGGCTGAGC 780  
AAAGAGGCAC TGATCCAGGC ACTGGGTGAG CCGGGGCCCT ACCTCCTGGC TGGAGAAGGC 840  
CCCCTGGACA AGGGGGAGTC CTGCGGCGGC GGTCGAGGGG AGCTGGCTGA GCTGCCCAAT 900  
GGGCTGGGGG AGACTCGGGG CTCCGAGGAC GAGACGGACG ACGATGGGGA AGACTTCACG 960  
CCACCCATCC TCAAAGAGCT GGAGAACCTC AGCCCTGAGG AGGCGGCCCA CCAGAAAGCC 1020  
GTGGTGGAGA CCCTTCTGCA GTAAGGAGCC CTGCCCCGTC CCCGCTCCCA GGAGAGCCTA 1080  
GAGGGGCCCC CCTCAGCTCC TAACGAGCCC CCCTTCTGAG TTGAGTCCCC ATGACCTTCA 1140  
GCCTTTAGCC TAGTTGCTGG GAAGGGGGAC AGGGCCCATG AGAGCCCAGG GGTCTTGCT 1200



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GAAAAAGCAG	TGAATTCACA	ACTCAAATGC	CCACCCACCC	ATCCATCCAT	CCGTCCATCC	1380
ACCCATTTCAT	CCATTTCATCC	ATTCACCCAT	CCATCCATCC	ACATATCTTC	ATCTGTGTTG	1440
TGTGTCTGTG	TATCCATGTT	TCTAAACCTT	TATCTGTTCC	AGTGTCTGTA	TCCATAGGCC	1500
TGTGTCCACG	TTTGTTCATGT	GTGTGCGTCN	ACAAGTCTCT	GTCCTCATGA	CCATGTGTCT	1560
GTGTCCCTGT	GTCCTGGCAT	AAATGACCAT	ACCTCACCGT	CCCTGAGTCT	ATGTGTAGGC	1620
CCCTGGGCTC	CATAACTGCT	TTCATGCACA	GTCCCCACCC	TCAGAGTTGA	CAAGGTTCCA	1680
GCACCCAGGA	CCGCAGCCCC	ACCTATGGGG	AGAGACAGCC	CTTGCTGAGC	AGATCCCGTC	1740
CTTGCCCTCT	CCCAGGGAGG	ACCCGTGGCG	TGTGGCGAAG	ATGGTCAAGT	CCTACCTGCA	1800
GCAGCACAA	ATCCCACAGC	GGGAGGTGGT	CGATAACCACT	GGCCTCAACC	AGTCCCACCT	1860
GTCCCAACAC	CTCAACAAGG	GCACTCCCAT	GAAGACGCAG	AAGCGGGCCG	CCCTGTACAC	1920
CTGGTACGTC	CGCAAGCAGC	GAGAGGTGGC	GCAGCGTAAG	TAATGACCCT	ACCCCGCATC	1980
TTCCCTGGGA	GGGCCCAGGA	CTCTCCCCTA	ACTCATAGGT	GGGGGCTGGA	AGCTTCACCA	2040
TCCCCATTAC	ACAGACAGGT	AGATGGAAAG	GAAGTCAGTG	GGATTCAACC	TGCATTTATT	2100
ACCTATTCTG	CGCCAGGCAC	TCTGTGGGAC	GGGAGTANAC	TTGGTCCTGA	ACATCCAAAG	2160
ATGAATGAAA	TGGGTCCCTG	CTTTCTTTTT	CTTTTTTTAG	ATACGTGACT	CTGGAAAAAT	2220
ATGTAAGCTC	TCTGAGCCTC	AGCTTCTTCA	TCTGTACAAT	GGGGATAGTA	AATGTGCCAA	2280
ATCAGAACAA	ATGCTAATGC	TTACCTGCAG	TCTTGTACTG	AGAAGGATGG	TGAGATCATA	2340
TCTTGGGTTG	GTAGGAAAGC	ATTCAGGGAT	TGATTAGTGA	TGTTTGCCCT	GAACACAGGT	2400
TAAGAAAGTG	ATGGCATGTG	TGCTGTGTGT	TTGTCATCAG	TAGATTAGAT	GATTTCTAAG	2460
TTCTAGCTGT	AAGCTCCTCT	GGTTCAGCGC	CATGGCAATG	AGAAAGAATC	AAGGGCAAGG	2520
TCAGGGGAAT	GGACGAGGGA	AGGTGAGAGT	GGCCAGTACC	CCACTCACGG	CTTTCTGTGC	2580
CTGCAGAGTT	CACCCATGCA	GGGCAGGGAG	GGCTGATTGA	AGAGCCCACA	GGTGATGAGC	2640
TACCAACCAA	GAAGGGGCGG	AGGAACCGTT	TCAAGTGGGG	CCCAGCATCC	CAGCAGATCC	2700
TGTTCCAGGC	CTATGAGAGG	CAGAAGAACC	CTAGCAAGGA	GGAGCGAGAG	GTACAACGGC	2760
GGGCGGGAAA	CAGTGCTGGT	TTGGTCTGGG	CTGCGGCAAG	GCCAGGGGAA	GGGGAAGGTG	2820
ACTCTAGGTC	CTGTAAAAGG	CTGTCCAGTT	GCCGAGAACT	CCTGATATTG	GCTTAGCCTG	2880

GCCCAGAAAA	TTGAGAATAC	TTGAACCTAA	GCCCATTCTCT	CGCAGCCCCC	CTGCACCNTG	2940
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GCTCTTTTGC	TCACTTTATG	AATGGAGAGA	CTGAGGTCAG	ACAGACTGTC	AATTGCCCAA	3060
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GNTCAGCTTC	TCAGAACCCT	CCCCTTCATG	CCCAGGACAG	GGTTCCTCTG	AGCCTGGCCT	3180
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CCAACCGGCG	CAAAGAAGAA	GCCTTCCGGC	ACAAGCTGGC	CATGGACACG	TACAGCGGGC	3360
CCCCCCCAGG	GCCAGGCCCG	GGACCTGCGC	TGCCCCGCTCA	CAGCTCCCCT	GGCCTGCCTC	3420
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GGGAAGGTGG	GAGGGTTGGG	GAGGACTGTC	CCATTGACAG	CAGTCACCTA	AACCTCTTTG	3540
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 <223> Description of Artificial Sequence: Synthetic Peptide

<400> 127

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Pro	Gly	Pro	Tyr	Leu	Leu	Ala	Gly	Glu	Gly	Pro	Leu	Asp	Lys	Gly	Glu	35	40	45	
Ser	Cys	Gly	Gly	Gly	Arg	Gly	Glu	Leu	Ala	Glu	Leu	Pro	Asn	Gly	Leu	50	55	60	
Gly	Glu	Thr	Arg	Gly	Ser	Glu	Asp	Glu	Thr	Asp	Asp	Asp	Gly	Glu	Asp	65	70	75	80
Phe	Thr	Pro	Pro	Ile	Leu	Lys	Glu	Leu	Glu	Asn	Leu	Ser	Pro	Glu	Glu	85	90	95	
Ala	Ala	His	Gln	Lys	Ala	Val	Val	Glu	Thr	Leu	Leu	Gln	Glu	Asp	Pro	100	105	110	
Trp	Arg	Val	Ala	Lys	Met	Val	Lys	Ser	Tyr	Leu	Gln	Gln	His	Asn	Ile	115	120	125	
Pro	Gln	Arg	Glu	Val	Val	Asp	Thr	Thr	Gly	Leu	Asn	Gln	Ser	His	Leu	130	135	140	
Ser	Gln	His	Leu	Asn	Lys	Gly	Thr	Pro	Met	Lys	Thr	Gln	Lys	Arg	Ala	145	150	155	160
Ala	Leu	Tyr	Thr	Trp	Tyr	Val	Arg	Lys	Gln	Arg	Glu	Val	Ala	Gln	Gln	165	170	175	
Phe	Thr	His	Ala	Gly	Gln	Gly	Gly	Leu	Ile	Glu	Glu	Pro	Thr	Gly	Asp	180	185	190	
Glu	Leu	Pro	Thr	Lys	Lys	Gly	Arg	Arg	Asn	Arg	Phe	Lys	Trp	Gly	Pro	195	200	205	
Ala	Ser	Gln	Gln	Ile	Leu	Phe	Gln	Ala	Tyr	Glu	Arg	Gln	Lys	Asn	Pro	210	215	220	
Ser	Lys	Glu	Glu	Arg	Glu	Thr	Leu	Val	Glu	Glu	Cys	Asn	Arg	Ala	Glu	225	230	235	240
Cys	Ile	Gln	Arg	Gly	Val	Ser	Pro	Ser	Gln	Ala	Gln	Gly	Leu	Gly	Ser				

245										250					255				
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			260					265					270						
Lys	Glu	Glu	Ala	Phe	Arg	His	Lys	Leu	Ala	Met	Asp	Thr	Tyr	Ser	Gly				
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Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Ser	Glu	Thr	Ala	Glu	Val	Pro	Ser	Ser				
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Pro	Thr	Gly	Leu	Glu	Pro	Ser	His	Ser	Leu	Leu	Ser	Thr	Glu	Ala	Lys				
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Thr	Leu	Val	Ile	Gly	Leu	Ala	Ser	Thr	Gln	Ala	Gln	Ser	Val	Pro	Val				
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Ser	Gln	Pro	Leu	His	Pro	Ser	Tyr	Gln	Gln	Pro	Leu	Met	Pro	Pro	Val				
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				485					490					495					
Gln	Ser	Pro	His	Ala	Leu	Tyr	Ser	His	Lys	Pro	Glu	Val	Ala	Gln	Tyr				
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Thr	His	Thr	Gly	Leu	Leu	Pro	Gln	Thr	Met	Leu	Ile	Thr	Asp	Thr	Thr				
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Asn	Leu	Ser	Ala	Leu	Ala	Ser	Leu	Thr	Pro	Thr	Lys	Gln	Val	Phe	Thr				
	530					535					540								
Ser	Asp	Thr	Glu	Ala	Ser	Ser	Glu	Ser	Gly	Leu	His	Thr	Pro	Ala	Ser				

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Gln	Ala	Thr	Thr	Leu	His	Val	Pro	Ser	Gln	Asp	Pro	Ala	Gly	Ile	Gln
				565					570					575	
His	Leu	Gln	Pro	Ala	His	Arg	Leu	Ser	Ala	Ser	Pro	Thr	Val	Ser	Ser
			580					585					590		
Ser	Ser	Leu	Val	Leu	Tyr	Gln	Ser	Ser	Asp	Ser	Ser	Asn	Gly	Gln	Ser
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His	Leu	Leu	Pro	Ser	Asn	His	Ser	Val	Ile	Glu	Thr	Phe	Ile	Ser	Thr
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TGGCTGATAA GCAGAACCAG TAAAAGAAGG TCTCTAGCCC CCCAGCGTGA GTACAATGGA	180
CCCTGGCAAA GCCCCGCTCC CGGCCAGGT CTTCTGCTCT CCAGGTCTGC CCCTCCGGCT	240
CTCCCTCTCT CCGGGTTTCC CCCTCCCCAC CATCATTTGC ATCCAGCCGA AAGCTGGGCC	300
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<211> 609

<212> PRT

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 129

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Leu	Ser	Ser	Gly	Val	Thr	Lys	Glu	Val	Leu	Val	Gln	Ala	Leu	Glu	Glu	20	25	30	
Leu	Leu	Pro	Ser	Pro	Asn	Phe	Gly	Val	Lys	Leu	Glu	Thr	Leu	Pro	Leu	35	40	45	
Ser	Pro	Gly	Ser	Gly	Ala	Glu	Pro	Asp	Thr	Lys	Pro	Val	Phe	His	Thr	50	55	60	
Leu	Thr	Asn	Gly	His	Ala	Lys	Gly	Arg	Leu	Ser	Gly	Asp	Glu	Gly	Ser	65	70	75	80
Glu	Asp	Gly	Asp	Asp	Tyr	Asp	Thr	Pro	Pro	Ile	Leu	Lys	Glu	Leu	Gln	85	90	95	
Ala	Leu	Asn	Thr	Glu	Glu	Ala	Ala	Glu	Gln	Arg	Ala	Glu	Val	Asp	Arg	100	105	110	
Met	Leu	Ser	Glu	Asp	Pro	Trp	Arg	Ala	Ala	Lys	Met	Ile	Lys	Gly	Tyr	115	120	125	
Met	Gln	Gln	His	Asn	Ile	Pro	Gln	Arg	Glu	Val	Val	Asp	Val	Thr	Gly	130	135	140	
Leu	Asn	Gln	Ser	His	Leu	Ser	Gln	His	Leu	Asn	Lys	Gly	Thr	Pro	Met	145	150	155	160
Lys	Thr	Gln	Lys	Arg	Ala	Ala	Leu	Tyr	Thr	Trp	Tyr	Val	Arg	Lys	Gln				

165										170					175				
Arg	Glu	Ile	Leu	Arg	Gln	Phe	Asn	Gln	Thr	Val	Gln	Ser	Ser	Gly	Asn				
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Met	Thr	Asp	Lys	Ser	Ser	Gln	Asp	Gln	Leu	Leu	Phe	Leu	Phe	Pro	Glu				
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Phe	Ser	Gln	Gln	Ser	His	Gly	Pro	Gly	Gln	Ser	Asp	Asp	Ala	Cys	Ser				
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Glu	Pro	Thr	Asn	Lys	Lys	Met	Arg	Arg	Asn	Arg	Phe	Lys	Trp	Gly	Pro				
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Ala	Ser	Gln	Gln	Ile	Leu	Tyr	Gln	Ala	Tyr	Asp	Arg	Gln	Lys	Asn	Pro				
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Ser	Lys	Glu	Glu	Arg	Glu	Ala	Leu	Val	Glu	Glu	Cys	Asn	Arg	Ala	Glu				
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Cys	Leu	Gln	Arg	Gly	Val	Ser	Pro	Ser	Lys	Ala	His	Gly	Leu	Gly	Ser				
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Asn	Leu	Val	Thr	Glu	Val	Arg	Val	Tyr	Asn	Trp	Phe	Ala	Asn	Arg	Arg				
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Lys	Glu	Glu	Ala	Phe	Arg	Gln	Lys	Leu	Ala	Met	Asp	Ala	Tyr	Ser	Ser				
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Gly	Val	Arg	Tyr	Ser	Gln	Gln	Gly	Asn	Asn	Glu	Ile	Thr	Ser	Ser	Ser				
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Thr	Ile	Ser	His	His	Gly	Asn	Ser	Ala	Met	Val	Thr	Ser	Gln	Ser	Val				
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Leu	Gln	Gln	Val	Ser	Pro	Ala	Ser	Leu	Asp	Pro	Gly	His	Asn	Leu	Leu				
		435					440					445							
Ser	Pro	Asp	Gly	Lys	Met	Ile	Ser	Val	Ser	Gly	Gly	Gly	Leu	Pro	Pro				
		450				455					460								
Val	Ser	Thr	Leu	Thr	Asn	Ile	His	Ser	Leu	Ser	His	His	Asn	Pro	Gln				

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Gln Ser Gln Asn Leu Ile Met Thr Pro Leu Ser Gly Val Met Ala Ile						
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Ala Gln Ser Leu Asn Thr Ser Gln Ala Gln Ser Val Pro Val Ile Asn						
	500		505			510
Ser Val Ala Gly Ser Leu Ala Ala Leu Gln Pro Val Gln Phe Ser Gln						
	515		520			525
Gln Leu His Ser Pro His Gln Gln Pro Leu Met Gln Gln Ser Pro Gly						
	530		535			540
Ser His Met Ala Gln Gln Pro Phe Met Ala Ala Val Thr Gln Leu Gln						
	545		550		555	560
Asn Ser His Met Tyr Ala His Lys Gln Glu Pro Pro Gln Tyr Ser His						
	565			570		575
Thr Ser Arg Phe Pro Ser Ala Met Val Val Thr Asp Thr Ser Ser Ile						
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Ser Thr Leu Thr Asn Met Ser Ser Ser Lys Gln Cys Pro Leu Gln Ala						
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Trp						
609						

<210> 130  
 <211> 10014  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Description of Artificial Sequence: Synthetic  
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CTCAAACCAC CCTTTGAAGT TGATTGTACA TTTTACAGAA AAGGAAACTG AGGCTCGGAG	240
AGGAGAATCA TTTACCCAAG GTCCCAGTTA GTAGACGGTA GGTGCCTGAA TGTAATCCA	300
GGTCTCTGCC TGCTCCGGGA GGGGGTGGGG GTGAGGGAAA CAGGAGAATG TGATGGGAAA	360
ATCCGAGATG GAGCCAGCCT GGGCCAGAAA CACTGGGAGC TGTGGGAGAC GGAGAGGGGC	420
AGGGTGGGAT CACAGGGAGC AGGAGCGGG AATTGGAGGT GAATCTGGCC CTCCCAAAC	480
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<210> 131

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<212> PRT

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic Peptide

<400> 131

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Val	Leu	Thr	Met	Gly	Asn	Gly	Pro	Ser	Ser	Pro	His	Cys	Leu	Thr	Val
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Ala	Leu	Leu	Gly	Ala	Trp	His	Ser	Asp	Met	Met	Ile	Leu	Leu	Pro	Leu
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 Asp Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Arg Lys Asn His Met  
 130 135 140  
 Tyr Ser Cys Arg Phe Ser Arg Gln Cys Val Val Asp Lys Asp Lys Arg  
 145 150 155 160  
 Asn Gln Cys Arg Tyr Cys Arg Leu Lys Lys Cys Phe Arg Ala Gly Met  
 165 170 175  
 Lys Lys Glu Ala Val Gln Asn Glu Arg Asp Arg Ile Ser Thr Arg Arg  
 180 185 190  
 Ser Ser Tyr Glu Asp Ser Ser Leu Phe Ser Ile Asn Ala Leu Leu Gln  
 195 200 205  
 Ala Glu Val Leu Ser Arg Gln Ile Thr Ser Pro Val Ser Gly Ile Asn  
 210 215 220  
 Gly Asp Ile Arg Ala Lys Lys Ile Ala Ser Ile Ala Asp Val Cys Glu  
 225 230 235 240  
 Ser Met Lys Glu Gln Leu Leu Val Leu Val Glu Trp Ala Lys Tyr Ile  
 245 250 255  
 Pro Ala Phe Cys Glu Leu Pro Leu Asp Asp Gln Val Ala Leu Leu Arg  
 260 265 270  
 Ala His Ala Gly Glu His Leu Leu Leu Gly Ala Thr Lys Arg Ser Met  
 275 280 285  
 Val Phe Lys Asp Val Leu Leu Leu Gly Asn Asp Tyr Ile Val Pro Arg  
 290 295 300  
 His Cys Pro Glu Leu Ala Glu Met Ser Arg Val Ser Ile Arg Ile Leu  
 305 310 315 320  
 Asp Glu Leu Val Leu Pro Phe Gln Glu Leu Gln Ile Asp Asp Asn Glu  
 325 330 335  
 Tyr Ala Tyr Leu Lys Ala Ile Ile Phe Phe Asp Pro Asp Ala Lys Gly  
 340 345 350  
 Leu Ser Asp Pro Gly Lys Ile Lys Arg Leu Arg Ser Gln Val Gln Val  
 355 360 365  
 Ser Leu Glu Asp Tyr Ile Asn Asp Arg Gln Tyr Asp Ser Arg Gly Arg  
 370 375 380

Phe Gly Glu Leu Leu Leu Leu Leu Pro Thr Leu Glu Ser Ile Thr Trp  
385 390 395 400  
Gln Met Ile Glu Gln Ile Gln Phe Ile Lys Leu Phe Gly Met Ala Lys  
405 410 415  
Ile Asp Asn Leu Leu Gln Glu Met Leu Leu Gly Gly Gly Pro Cys Gln  
420 425 430  
Ala Gln Glu Gly Arg Gly Trp Ser Gly Asp Ser Pro Gly Asp Arg Pro  
435 440 445  
His Thr Val Ser Ser Pro Leu Ser Ser Leu Ala Ser Pro Leu Cys Arg  
450 455 460  
Phe Gly Gln Val Ala Gly Ser Pro Ser Asp Ala Pro His Ala His His  
465 470 475 480  
Pro Leu His Pro His Leu Met Gln Glu His Met Gly Thr Asn Val Ile  
485 490 495  
Val Ala Asn Thr Met Pro Thr His Leu Ser Asn Gly Gln Met Cys Glu  
500 505 510  
Trp Pro Arg Pro Arg Gly Gln Ala Ala Thr Pro Glu Thr Pro Gln Pro  
515 520 525  
Ser Pro Pro Gly Gly Ser Gly Ser Glu Pro Tyr Lys Leu Leu Pro Gly  
530 535 540  
Ala Val Ala Thr Ile Val Lys Pro Leu Ser Ala Ile Pro Gln Pro Thr  
545 550 555 560  
Ile Thr Lys Gln Glu Val Ile  
565

<210> 132

<211> 470

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 132

AAGTAAGCCT TGT TTTTCCA CACTCATTCT CCCAGGTTTT CTTTGGATAG GCTTACTTTT	60
CCATGCTGGA GGAGGGGCTA TCCCTTCATT TTGCCTCTCC CGCTTCCCTC CCTCTCCCCC	120
TCCCCCTGCT TTCTCTCCCT CTGCACTTTG TGAAGTCTG CTGCAGTGCT GAAGTCCAAA	180
GTTCAAGTAAC TTGCTAAGCA CACAGATAAA TATGAACCTT GGAGAATTTA CCAATGTAAA	240
CAGATAGCCA AGGGTCCCTT TATCAGCACT GGCTCAGGAC AGTCGTGGGG GGTCTGAAGT	300
GGCTCAATTT TGTATTTTGT TTTTTTTGGG GGGGTGTAAA GCGGGGAGGC TCGCTGTGC	360

CCGCTGCTGA CAGTCGGGCG TGTACCTCG GGAACATGGT GTAGGGAAGC TGAAGCAGG 420

ATAACGTGGA ACTCAACCCA AGAAACGCCA GCCTGAAGAC CATGGTCTCG 470

<210> 133

<211> 467

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 133

TCACAGCTAT TAGCTCATCG CTGCCAAATT GCCCCTTTAC CTAGGCTTGT GTCACTTTCA 60

CCTTCTCATT CTCTTACTTT TACATTCTTC CTTGATATTT TGCTTTTTTCA ACTTTTGGAA 120

ATTTCTTTCT CTCTTCTACC CCTCCTCATA TTCCTCTGCA CTCCCCCTC TCTAACTCAT 180

GCACTTTGTG GGGTCCAAAG TTCAGTAACT TGCAAAGCAC AGGGATAAAG ATGAACCTTG 240

GAAGATTTAC TCTGCTCTGA TGTAAACAGA GAGTGACAAG GGTCCCTTAT CTATGTCTCA 300

GAGAAGCCTG TCCGGGGGGT GACCACTTGC TGGTTGTGGC TGCACAGTGT GTTTTTTTGG 360

GGGGGAGGAG GAAACAGAAG GTGGGTAGAG CATGGACTCC CGCCCGCTGA TCCGTGTTAC 420

AGCCGCAGAT GGTGAGGCAG TAGAAGGCAA CAGACAGGAT GCGCTCT 467

<210> 134

<211> 479

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 134

TTTCGGGGGT GGGACCCAAC GCTGCTCTCC TGATGGCCTC CCTGGCTCCC AGCACCTTCC 60

ATCCCAGCTG CTCAGGGCCC CTCACCTGCG CCTCCCCAC CCTCCCCTCT GCCCACTCCC 120

ATCGCAGGCC ATAGCTCCCT GTCCCTCTCC GCTGCCATGA GGCCTGCACT TTGCAGGGCT 180

GAAGTCCAAA GTTCAGTCCC TTCGCTAAGC ACACGGATAA ATATGAACCT TGGAGAATTT 240

CCCCAGCTCC AATGTAAACA GAACAGGCAG GGGCCCTGAT TCACGGGCCG CTGGGGCCAG 300

GGTTGGGGGT TGGGGGTGCC CACAGGGCTT GGCTAGTGGG GTTTTGGGGG GGCAGTGGGT 360

GCAAGGAGTT TGGTTTGTGT CTGCCGGCCG GCAGGCAAAC GCAACCCACG CGGTGGGGGA 420

GGCGGCTAGC GTGGTGGACC CGGGCCGCGT GGCCCTGTGG CAGCCGAGCC ATGGTTTCT 479

<210> 135

<211> 605  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 135  
 TGGGGCCTGG GATTTAGGTT TCTAAATCGT GGGCCATGGG GCAGCCTTAT CTCTGCAAAA 60  
 GCATTGAGGG TAGAAGTCAA TGATTTGGGA AGTTATTGAA TTAGGGGATC TCGGAGGTAG 120  
 GCTGTCAGTG CCTGATAGTA TCAGTTAGAA TGCCTGACTT GGGGTGACAA TGGCTTGGAG 180  
 GGGTGGGTGA GTCAAGGGTC AAATGAGTGC CCGTGAGTCA TGATGCCTGC CTTGTACAAT 240  
 TGATAACTGA ACATCGGTGA GTTAGGGCCC CAGCAGTTGT AATTAGCACC CCGGGTGTCA 300  
 GCCAGAAACC AACAAACAGC CAAATCCCTG CAGCCCCGCC CAGCCTATCC ACCGGCGGGG 360  
 GACCGATTAA CCATTAACCC CCACCCCTCC CCGGCAGAGC CTCCACCCCT TCACAGAGGC 420  
 TAGGCCAAGA CTCCAGCAG ATCTTCCAG AGGACGGTTT GAAAGGAAGG CAGAGAGGGC 480  
 ACTGGGAGGA GGCAGTGGGA GGGCGGAGGG CGGGGGCCTT CGGGGTGGGC GCCCAGGGTA 540  
 GGGCAGGTGG CCGCGGCGTG GAGGCAGGGA GAATGCGACT CTCCAAAACC CTCGTCGACG 600  
 ACATG 605

<210> 136  
 <211> 478  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 136  
 TCCTGGAGAG TGGGACCCAG CGCCGCACCC AGAGGCCTCC TGGCTCCTGC TGCCTCTAGC 60  
 CCTGCGCCCC TGGCCCCTCT CCACCTCCCC CACCCTCCCT TCTGCTCACT CCCAATTGCA 120  
 GGCCATGACT CCGGTCCGCG TCCCTCTCAC CCCCATGAGG CCTGCACTTG CAAGGCTGAA 180  
 GTCCAAAGTT CAGTCCCTTC GCTAAGCGCA CGGATAAATA TGAACCTTGG AGAATTTCCC 240  
 CAGCTCCAAT GTAAACAGAG CAGGCAGGGG CCCTGATTCA CTGGCCGCTG GGGCCAGGGT 300  
 TGGGGGCTGG GGGTGCCAC AGAGCTTGAC TAGTGGGATT TGGGGGGGCA GTGGGTGCAG 360  
 CGAGCCCGGT CCGTTGACTG CCAGCCTGCC GGCAGGTAGA CACCGGCCGT GGGTGGGGGA 420  
 GGCGGCTAGC TCAGTGGCCT TGGGCCGCGT GGCTGGTGGC AGCGGAGCCA TGGTTTCT 478

<210> 137

<211> 622  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 137  
 TGGGCTTGGG TGTTAGGTTT CCAGTTCAAG CGACCCAGGA CAGCTTTATC TCAAATTGAG 60  
 GATAGAAGTC AATGATCTGG GACGTGATTG GCTTAGGGCT TCATAGTGGT AGGCTTGCCA 120  
 GTGTCTAAAC ATGTCAGCTG GGTGTCCAC CTTGGTGAGA CTTGGGGGCT GCTGAGGCAA 180  
 GGGGTCCAAC CAATGCCAGT CCTGTTGGGT GCCTGCCTTG GAAGATTGGT AAGTGA CTAT 240  
 TAATGAGCGG GAGGTGGGGG GGGGGCAACA GTTGTAAATTA GCACCCAGG TGTCAGTCAG 300  
 AAACCAACAA ACAGCCAAAT CCTCGTGGCT CCACCCAGCC TACCCAGCAA CGGGGGTGAT 360  
 TAACCATTAA CTCCTACCCC TCCCCACAGA GCCTCCACCC TCTGCAGAGG CTAGGCCAGG 420  
 ACGCCAGGCT GAGTCTCCCA GAGGACAGTT TGAAAGAGAG GAAGGCAGAG AAGGGACCTG 480  
 GGAGGAGGCA GGAGGAGGGC GGGGACGGGG GGGGCTGGGG CTCAGCCCAG GGGCTTGGGT 540  
 GGCATCCTGG GCCGGGCAGG ACAGGGGGCT AAGGCGTGGG TAGGGGAGAA TGC GACTCTC 600  
 TAAAACCTT GCCGGCGATA TG 622

<210> 138  
 <211> 470  
 <212> DNA  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 138  
 TCTTGGGCAG TGGGACCAGC GCTGCTCCCA GAGGCCTCCT GGCTCCTGGT GCCTCTCTCC 60  
 CTGCGCCCCT GGTTCCTGCT CCACCTCCCC CACCCGCCCT TCTGCTCACT CCCAATTGCA 120  
 AGCCATGGCT CCCGGTCCGG TCCCTCTCGC TGCTGTGAGG CCTGCACTTG CAAGGCTGAA 180  
 GTCCAAAGTT CAGTCCCTTC GCTAAGCACA CGGATAAATA TGAACCTTGG AGAATTTCCC 240  
 CAGCTCCAAT GTAAACAGAG CAGCAGGGGG CCCTGATTCA CTAGCCGCTG GGGCCAGGGT 300  
 TGGGGGTTGG GGGTGCCAC AGGGCTTGAC TAGTGGGATT TGGGGGAGCA GTGGGTGCAG 360  
 CGAGCCTGGT CCGTTGACTG CCAGCAGTAG ACACCGGCCG TGTGTGGGGG AGGCGGCTAG 420  
 CTCAGTGGCC TTGGGCCGCG TGGCCTGGCG GTAGAGGAGC CATGGTTTCT 470

<210> 139

<211> 557  
 <212> PRT  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Peptide

<400> 139

Met	Val	Ser	Lys	Leu	Thr	Ser	Leu	Gln	Gln	Glu	Leu	Leu	Ser	Ala	Leu	1	5	10	15
Leu	Ser	Ser	Gly	Val	Thr	Lys	Glu	Val	Leu	Val	Gln	Ala	Leu	Glu	Glu	20	25	30	
Leu	Leu	Pro	Ser	Pro	Asn	Phe	Gly	Val	Lys	Leu	Glu	Thr	Leu	Pro	Leu	35	40	45	
Ser	Pro	Gly	Ser	Gly	Ala	Glu	Pro	Asp	Thr	Lys	Pro	Val	Phe	His	Thr	50	55	60	
Leu	Thr	Asn	Gly	His	Ala	Lys	Gly	Arg	Leu	Ser	Gly	Asp	Glu	Gly	Ser	65	70	75	80
Glu	Asp	Gly	Asp	Asp	Tyr	Asp	Thr	Pro	Pro	Ile	Leu	Lys	Glu	Leu	Gln	85	90	95	
Ala	Leu	Asn	Thr	Glu	Glu	Ala	Ala	Glu	Gln	Arg	Ala	Glu	Val	Asp	Arg	100	105	110	
Met	Leu	Ser	Glu	Asp	Pro	Trp	Arg	Ala	Ala	Lys	Met	Ile	Lys	Gly	Tyr	115	120	125	
Met	Gln	Gln	His	Asn	Ile	Pro	Gln	Arg	Glu	Val	Val	Asp	Val	Thr	Gly	130	135	140	
Leu	Asn	Gln	Ser	His	Leu	Ser	Gln	His	Leu	Asn	Lys	Gly	Thr	Pro	Met	145	150	155	160
Lys	Thr	Gln	Lys	Arg	Ala	Ala	Leu	Tyr	Thr	Trp	Tyr	Val	Arg	Lys	Gln	165	170	175	
Arg	Glu	Ile	Leu	Arg	Gln	Phe	Asn	Gln	Thr	Val	Gln	Ser	Ser	Gly	Asn	180	185	190	
Met	Thr	Asp	Lys	Ser	Ser	Gln	Asp	Gln	Leu	Leu	Phe	Leu	Phe	Pro	Glu	195	200	205	
Phe	Ser	Gln	Gln	Ser	His	Gly	Pro	Gly	Gln	Ser	Asp	Asp	Ala	Cys	Ser	210	215	220	
Glu	Pro	Thr	Asn	Lys	Lys	Met	Arg	Arg	Asn	Arg	Phe	Lys	Trp	Gly	Pro	225	230	235	240
Ala	Ser	Gln	Gln	Ile	Leu	Tyr	Gln	Ala	Tyr	Asp	Arg	Gln	Lys	Asn	Pro	245	250	255	



Ser Lys Glu Glu Arg Glu Ala Leu Val Glu Glu Cys Asn Arg Ala Glu  
 260 265 270  
 Cys Leu Gln Arg Gly Val Ser Pro Ser Lys Ala His Gly Leu Gly Ser  
 275 280 285  
 Asn Leu Val Thr Glu Val Arg Val Tyr Asn Trp Phe Ala Asn Arg Arg  
 290 295 300  
 Lys Glu Glu Ala Phe Arg Gln Lys Leu Ala Met Asp Ala Tyr Ser Ser  
 305 310 315 320  
 Asn Gln Thr His Ser Leu Asn Pro Leu Leu Ser His Gly Ser Pro His  
 325 330 335  
 His Gln Pro Ser Ser Ser Pro Pro Asn Lys Leu Ser Gly Val Arg Tyr  
 340 345 350  
 Ser Gln Gln Gly Asn Asn Glu Ile Thr Ser Ser Ser Thr Ile Ser His  
 355 360 365  
 His Gly Asn Ser Ala Met Val Thr Ser Gln Ser Val Leu Gln Gln Val  
 370 375 380  
 Ser Pro Ala Ser Leu Asp Pro Gly His Asn Leu Leu Ser Pro Asp Gly  
 385 390 395 400  
 Lys Met Ile Ser Val Ser Gly Gly Gly Leu Pro Pro Val Ser Thr Leu  
 405 410 415  
 Thr Asn Ile His Ser Leu Ser His His Asn Pro Gln Gln Ser Gln Asn  
 420 425 430  
 Leu Ile Met Thr Pro Leu Ser Gly Val Met Ala Ile Ala Gln Ser Leu  
 435 440 445  
 Asn Thr Ser Gln Ala Gln Ser Val Pro Val Ile Asn Ser Val Ala Gly  
 450 455 460  
 Ser Leu Ala Ala Leu Gln Pro Val Gln Phe Ser Gln Gln Leu His Ser  
 465 470 475 480  
 Pro His Gln Gln Pro Leu Met Gln Gln Ser Pro Gly Ser His Met Ala  
 485 490 495  
 Gln Gln Pro Phe Met Ala Ala Val Thr Gln Leu Gln Asn Ser His Met  
 500 505 510  
 Tyr Ala His Lys Gln Glu Pro Pro Gln Tyr Ser His Thr Ser Arg Phe  
 515 520 525  
 Pro Ser Ala Met Val Val Thr Asp Thr Ser Ser Ile Ser Thr Leu Thr  
 530 535 540  
 Asn Met Ser Ser Ser Lys Gln Cys Pro Leu Gln Ala Trp  
 545 550 555

<210> 140  
 <211> 516  
 <212> PRT  
 <213> Artificial Sequence  
 <200>  
 <223> Description of Artificial Sequence: Synthetic  
 Peptide

<400> 140

Met	Asp	Met	Ala	Asp	Tyr	Ser	Ala	Ala	Leu	Asp	Pro	Ala	Tyr	Thr	Thr	1	5	10	15
Leu	Glu	Phe	Glu	Asn	Val	Gln	Val	Leu	Thr	Met	Gly	Asn	Gly	Pro	Ser	20	25	30	
Ser	Pro	His	Cys	Leu	Thr	Val	Ala	Leu	Leu	Gly	Ala	Trp	His	Ser	Asp	35	40	45	
Met	Met	Ile	Leu	Leu	Pro	Leu	Arg	Leu	Ala	Arg	Leu	Arg	His	Pro	Leu	50	55	60	
Arg	His	His	Trp	Ser	Ile	Ser	Gly	Gly	Val	Asp	Ser	Ser	Pro	Gln	Gly	65	70	75	80
Asp	Thr	Ser	Pro	Ser	Glu	Gly	Thr	Asn	Leu	Asn	Ala	Pro	Asn	Ser	Leu	85	90	95	
Gly	Val	Ser	Ala	Leu	Cys	Ala	Ile	Cys	Gly	Asp	Arg	Ala	Thr	Gly	Lys	100	105	110	
His	Tyr	Gly	Ala	Ser	Ser	Cys	Asp	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	115	120	125	
Ser	Val	Arg	Lys	Asn	His	Met	Tyr	Ser	Cys	Arg	Phe	Ser	Arg	Gln	Cys	130	135	140	
Val	Val	Asp	Lys	Asp	Lys	Arg	Asn	Gln	Cys	Arg	Tyr	Cys	Arg	Leu	Lys	145	150	155	160
Lys	Cys	Phe	Arg	Ala	Gly	Met	Lys	Lys	Glu	Ala	Val	Gln	Asn	Glu	Arg	165	170	175	
Asp	Arg	Ile	Ser	Thr	Arg	Arg	Ser	Ser	Tyr	Glu	Asp	Ser	Ser	Leu	Phe	180	185	190	
Ser	Ile	Asn	Ala	Leu	Leu	Gln	Ala	Glu	Val	Leu	Ser	Arg	Gln	Ile	Thr	195	200	205	
Ser	Pro	Val	Ser	Gly	Ile	Asn	Gly	Asp	Ile	Arg	Ala	Lys	Lys	Ile	Ala	210	215	220	
Ser	Ile	Ala	Asp	Val	Cys	Glu	Ser	Met	Lys	Glu	Gln	Leu	Leu	Val	Leu	225	230	235	240

Val Glu Trp Ala Lys Tyr Ile Pro Ala Phe Cys Glu Leu Pro Leu Asp  
 245 250 255  
 Asp Gln Val Ala Leu Leu Arg Ala His Ala Gly Glu His Leu Leu Leu  
 260 265 270  
 Gly Ala Thr Lys Arg Ser Met Val Phe Lys Asp Val Leu Leu Leu Gly  
 275 280 285  
 Asn Asp Tyr Ile Val Pro Arg His Cys Pro Glu Leu Ala Glu Met Ser  
 290 295 300  
 Arg Val Ser Ile Arg Ile Leu Asp Glu Leu Val Leu Pro Phe Gln Glu  
 305 310 315 320  
 Leu Gln Ile Asp Asp Asn Glu Tyr Ala Tyr Leu Lys Ala Ile Ile Phe  
 325 330 335  
 Phe Asp Pro Asp Ala Lys Gly Leu Ser Asp Pro Gly Lys Ile Lys Arg  
 340 345 350  
 Leu Arg Ser Gln Val Gln Val Ser Leu Glu Asp Tyr Ile Asn Asp Arg  
 355 360 365  
 Gln Tyr Asp Ser Arg Gly Arg Phe Gly Glu Leu Leu Leu Leu Pro  
 370 375 380  
 Thr Leu Glu Ser Ile Thr Trp Gln Met Ile Glu Gln Ile Gln Phe Ile  
 385 390 395 400  
 Lys Leu Phe Gly Met Ala Lys Ile Asp Asn Leu Leu Gln Glu Met Leu  
 405 410 415  
 Leu Gly Gly Ser Pro Ser Asp Ala Pro His Ala His His Pro Leu His  
 420 425 430  
 Pro His Leu Met Gln Glu His Met Gly Thr Asn Val Ile Val Ala Asn  
 435 440 445  
 Thr Met Pro Thr His Leu Ser Asn Gly Gln Met Cys Glu Trp Pro Arg  
 450 455 460  
 Pro Arg Gly Gln Ala Ala Thr Pro Glu Thr Pro Gln Pro Ser Pro Pro  
 465 470 475 480  
 Gly Gly Ser Gly Ser Glu Pro Tyr Lys Leu Leu Pro Gly Ala Val Ala  
 485 490 495  
 Thr Ile Val Lys Pro Leu Ser Ala Ile Pro Gln Pro Thr Ile Thr Lys  
 500 505 510  
 Gln Glu Val Ile  
 515

<210> 141  
 <211> 17  
 <212> DNA

<213> Artificial Sequence  
<200>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 141  
GCGGGACCGG ATCAGCA

17

<210> 142  
<211> 5  
<212> PRT  
<213> Artificial Sequence  
<200>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 142  
Arg Asp Arg Ile Ser  
1 5

<210> 143  
<211> 17  
<212> DNA  
<213> Artificial Sequence  
<200>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 143  
GCGGGACTGG ATCAGCA

17

<210> 144  
<211> 7  
<212> PRT  
<213> Artificial Sequence  
<200>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 144  
Ala Glu Val Leu Ser Arg Gln  
1 5

<210> 145  
<211> 30  
<212> DNA  
<213> Artificial Sequence  
<200>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<221> modified\_base  
<222> (16)

<223> N = C or T

<400> 145

GCGGAGGTCC TGTCNGACA GGTACCGGGG

30

<210> 146

<211> 15

<212> DNA

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> modified\_base

<222> (8)

<223> N = C or T

<400> 146

AAAGCAANGA GAGAT

15

<210> 147

<211> 4

<212> PRT

<213> Artificial Sequence

<200>

<223> Description of Artificial Sequence: Synthetic  
Peptide

<220>

<221> modified\_site

<222> (3)

<223> X = R or any amino acid

<400> 147

Lys Gln Xaa Glu

1